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gb_pr:AF089090
gb_pat:AR153294
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gb_pat:AX072472
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gb_ro:AF203031
                                                                                                                                                                                                                                                                                                                                                                                                                                  9b_htg:AC080022
9b_pr:AF158748
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gb_pat:AR153293
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Query: US-09-768-877-2
Query length: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pr:AK027330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pr:AF089091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_ro:AF126867
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Database length: 1873333701
Search time (sec): 2930.000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: Sep 17,
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-Q-/cgn2_1/USPTO_spool_US09768877/runat_16092002_152811_8346/app_query.fasta_1.739
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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
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-MINLEN=0 -MAXLEN=200000000 -USER-USO9768977_@CGN1_1.8402
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLEXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-768-877-2 to: GenEmbl:*
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. 4e-22
                                                                                                                                                                                     1.1e-51
1.6e-23
5.2e-23
1.7e-22
1.4e-23
                                                                                                                                                                                                                                                                                                                                                                                               .8e-84
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AB072744 Macaca fascicularis
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gb_pat:AX090205
gb_pat:AX063615
gb_pr:HSA242832
gb_pat:AX090213
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MEDLINE
REFERENCE
AUTHORS
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AUTHORS
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SOURCE
                                                                                                        alignment_scores:
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LOCUS AB058748
DEFINITION Homo sapiens
ACCESSION AB058748
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             Percent Similarity:
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      Quality: 3649.00
Ratio: 5.430
milarity: 100.000
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                                                                                                                                                                                                                                                    438
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<1. .2119
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644.50
644.50
644.50
644.50
Length: 672
Gaps: 0
Percent Identity: 100.000
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Direct Submission Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Rsearch Institute, Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Rsearch Institute, Submitted (37-MAR-2001) Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdhainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913, Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase,T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 8 (2), 85-95 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA for KIAA1845 protein, partial cds. AB058748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens brain cDNA to mRNA, clone: fg05317 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          /product="KIAA1845 protein"

/protein_id="BAB47474.1"

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/protein_id="BAB47474.1"

/db_xref="Gi:14017907"

/translation="GrGGPEAAAADSPSLRGCDPEATGCRWEPAEPRWRAGRGATPAR

ELFEDAAFPAADSSLFCDLSTPLAGPREDITWRRPQEICATPALFPDDPREGQVKQGL

LGDCWFLCACAALQKSRHLLDQVIPPGGPSWADADSYRGSFTCRIWQFGRWVEVTTDDR

LPCLAGRICFSRCQREDVFWLPLLEKVVAKVHGSYEHLWAGQVADALVDLTGGLAERW

LLGLAGRICFSRCQREDVFWLPLLEKVVAKVHGSYEHLWAGQVADALVDLTGGLAERW

RLKGVAASGGQODRPGRWEHRTCROLLHIKDQCLISCCVLSPRAGARELGEHAFIVS

DLRELQGAGQCILLARIQNPWGRRCWGGLWREGGEGWSQVDAAVASELLSQLOEGEF

WYEEEEFLREFDELTVGYFVTEAGHLOSLYTEKLLCHTRALFQAWYKGQSAGCCRNNS

GFPSNPKFWLFWSEPSHYITATLQRSELHAADWAGRARALVGDSHTSWSPASIPGKHY

CAVITATE WYEEDENLY INDUCKMINGTON TO THE WYE
SIHSQEMLGQFLQEVSVMAVMKT"
1 795 c 862 g 44
                                                                                                                                             QAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLK
DAPGEFLLRVFSTGRVSLSAIRAVAKNTTPGAALPAGEWGTVQLRGSWRVGQTAGGSR
NFASYPTNPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Start codon is not identified. fg05317 cDNA clone for KIAA1845 has 921-bp, 1755-bp, 495-bp and 1014-bp insertions after the positions 570, 788, 930 and 1378 of the sequence of KIAA1845, respectively."
                                                                                                   PPLLLQEPLLSCVPHRYAQEVSRLCLLPAGTYKVVPSTYLPDTEGAFTVTIATRIDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="fg05317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="vector:pBluescriptII SK plus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="brain"
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3.7e-22
3.9e-22
3.9e-22
4.8e-22
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2220
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AX090205
AX063615
AJ242832
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Sequence 1 from
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Sequence 9 from
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x AB058748 alignment\_block: US-09-768-877-2

to: 2536 from: 1 Align seg 1/1 to: AB058748

- 17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL
- - nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL

- - 134 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150

- GlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspGl GGCGGCTGGGAGCACAGGACTTGTCGGCAGCTGCTCCACCTGAAGGACCA
- nCysLeulleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL
- euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly

284	alAspAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 300	8
951		1000
301	PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 317	17
1001	TTCTGGGTGGAGGAGGAGTTCCTCAGGGAGTTTGACGAGCTCACGT	1050
317	lGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 334	34
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334	rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 350	20
1101	GCTGCTCTGCCATACGCGGGCGCTGGGGGCCTGGGGTCAAGGGCCCAG 1150	150
351	SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 367	23
1151	TCAGCAGGAGGCTGCCGGAACAACAGCGGCTTTCCCAGCAACCCCAAATT 1200	002
367	eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlaA 384	34
1201	CTGGCTGCGGGTCTCAGAACCGAGTGAGGTGTACATTGCCGTCCTGCAGA 1250	550
384	rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 400	0
1251	GATCCAGGCTGCACGCGCGGACTGGCCAGGCCGGGCCCGGGCACTGGTG 1300	00
401	GlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisTy 417	7
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1351	CCAGGCTGTGGGTCTGCACCTCTGGGAAGGTAGAAGCGGCGGGTCAATC 1400	00
434	euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450	0
1401	TCCTAGGGTCCTGTCCATGCCCCCCGTGGCTGGCACCGCGTGCCATGCA 1450	20
451	TyraspargGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe 467	2.
1451	TACGACCGGGAGGTCCACCTGCGTTGTGAGCTCTCACCGGGCTACTACCT 1500	00
467	uAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuA 484	4

1501 GGCTGTCCCCAGCACCTTCCTGAAGGACGCGCCAGGGGAGTTCCTGCTCC rgValPheSerThrGlyArgValSerLeuSerAlalleArgAlaValAla OSERASPTATGUPHEHISPROILEGLYPHEHISILEPHEGLUVALPROG snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu 

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FEATURES
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAGGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrGluGlyAlaPheThrValThrIleAlaThrArģTleAspArgProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_pr:BC004260
                                                                                               This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OR analysis, GenomeScan gene prediction.
                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 13 Row: a Column: 11
                                                                                                                                                                                                                                                                Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacquelline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2614 bp mRNA linear PRI 12-JUL-2001 Complete cds.
BC004260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2614)
                                                                                                                                                                                                                                                                                                                                                                                                                                           BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC004260.1 GI:13279049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: BC004260
                                                                                               134
                                                                                                                                        496
                                                                                                                                                                                                                         446
                                                                                                                                                                                                                               101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117
                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                           396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl
                                                                 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
                                                                                                                                                   yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134
                                                                                                                           ACGCTGGGTGGAGGTGACCACAGATGACCGCCTGCCGTGCCTTGCAGGGA
                                                                                                                                                                                                              GCCGACCAGGAGTACCGGGGCTCCTTCACCTGTCGCATTTGGCAGTTTGG
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alignment\_block: US-09-768-877-2 x BC004260 Percent Similarity: 100.000 Quality: 3649.00 Percent Identity: 672 0 100.000

from: 1 to: 2614

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595

545

us-09-768-877-2.rge

1496 TACGACCGGGAGGTCCACCTGCGTTGTGAGCTCTCACCGGGCTACTACCT 1545

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64	184	200	217	234	250 895	267 945	284 995	300 104	317 109	334 114	350 119	367 124	<b>384</b> 129	400 134	417	434 144	149	467
CIGGAAAAGGICTACGCCAAGGICCATGGGICCTACGAGCACCTGIGGG	aG1yG1nya1A1aAspA1aLeuVa1AspLeuThrG1yG1yLeuA1aG1uA 	rgTrpasnLeuLysGlyValAlaGlySerGlyGlyGlnGlnaspargPro 	GlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspGl 	nCysLeulleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL 	euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 	GInAlaGlyGlnCysIleLeuLeuLeuargIleGlnAsnProTrpGlyAr 	gArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnV 	alaspalaalavalalaseroluLeuLeuSerGlnLeuGlnGluGlyGlu 	PherrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 	1GlytyrProvalThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 	rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 	SeralagiygiycysargasnasnsergiypheproserasnproLysph 	efrpLeuArgValSerGlübroSerGlüValTyrIleAlaValLeuGlüA 	rgSerargLeuhisalaalaaspTrpalag°yargalaargalaleuval 	GlyaspSerHisThrSerTrpSerProalaSerIleProGlyLysHisTy 	rGlnalavalGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL 	euProArgValLeuSerMetProProValAlaGlyThrAlacysHisAla 	TyraspargGluValHisbeuargCysGluLeuSerProGlyTyrTre 
596	167	184	201	217	234	251 896	267	284	301	317 1096	334	351 1196	367	384	401	417	434	451

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PRI 12-JUL-2001
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1 (bases 1 to 2614)
Strausberg,R.
Direct Submission
Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS
BC007553
DEFINITION HOMO sapiens, clone IMAGE:2967328, mRNA, partial cds.
ACCESSION BC007553.
VERSION BC007553.1 GI:14043130
                                             2095
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                                                                                                                                               534
                                                                                                                                                                                                                                                                                         567 oSerAspThrGluPheHisProIleGlyPheHisIlePheGlnValProG 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650
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                                                                                                                                                                                                                                                                                                                                                                                    601 LeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysLe
                                                                                              501 LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2146 GGCAGTGATGAAACC 2161
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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REMARK

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alignment_block:
US-09-768-877-2 x BC007553
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Ratio: 5.430
Percent Similarity: 100.000
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196 CGCCTTCCCCGCCGCACTCCTCGCTCTTCTGCGACTTGTCTACGCCGC
                                                                                                                                                                                                                                            CDS
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                                                                                                                                                       17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                                                                                                                                                                                                                               1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17
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Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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Tissue Procurement: ATCC/DCTD/DTP
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Contact: MGC help desk
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PAT 08-AUG-2001
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Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I. and Cox,N.J.
Polynucleotides encoding calpain 10
Patent: US 6235481-A 3 22-MAY-2001;
Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
FEATURES
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REFERENCE AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases 1 to 2620)
Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del Bosque-Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S.,

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

VERSION KEYWORDS

ACCESSION DEFINITION

AF089088

sapiens calpain-like protease GI:10503934

mRNA CAPN10a

linear

r PRI 23

23-JAN-2001

AF089088.1

SOURCE

ORGANISM

Homo sapiens

seq\_documentation\_block:
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                                                                                                   2 (bases 1 to 2620)
Horikawa,Y. and Bell,G.I.
Direct Submission
Submitted (02-SEP-1998) Howard Hughes Medical Institute, The
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL
60637, USA
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Polonsky, K.S., Wei, S., Concannon, P., Iwasaki, N., Schulze, J.,
Baier, L.J., Bogardus, C., Groop, L., Boerwinkle, E., Hanis, C.L. and
                                                 is associated
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                                                the gene encoding calpain-10 mellitus
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Percent Similarity: 100.000 Percent Identity: 100.000
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178. .2194
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                                                             with type 2 diabetes mellitus
Nat. Genet. 26 (2), 163-175 (2000)
20472315
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US-09-768-877-2 x AF089088
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Sequence 13 from

patent

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DNA

PAT 08-AUG-2001

184

579 183

200

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ACCESSION
VERSION
KEYWORDS
SOURCE
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US-09-768-877-2 x AR153295
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Percent Similarity:
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             151 LeuGluLysValTyrAlaLys.ValHisGlySerTyrGluHisLeuTrpA 167
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                                                                                                                                   yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA
                                                                                                                                                                                                                                                                     ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp
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Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I.
Polynucleotides encoding calpain 10
Patent: US 6235481-A 13 22-MAY-2001;
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217 679 233	729 250 779 267 829	283 879 300 929 317	0 10 0	67 112 117 00	1229 417 1279 433 1329	450 1379 467 1429	483 1479 500 1529
		rgArgCySTrpGlnGlyLeuTrpArgGluGlyGlyGlyGluGlyTrpSerGln	alGlyTyrProValThrGlualaGlyHisLeuGlnSerLeuTyrThrGluillillillillillillillillillillillillil	O. nSerAlaGlyGlyCySArgAsnAsinSerGlyPheProSerAsnProLySP	ATCCAGGCTGCACGGGCAGTGGGCAGGCCGGGCCCGGGCACTGG !YASPSETH1SThrSetTrpSetProAlaSer11eProGlyLySH1S 	4 LeuProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAl 	7 eualavalproSerThrPheLeuLysAspAlaProGlyGluPheLeuLeu 
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Homo sapiens calpain-like protease CAPNIOf mRNA, complete cds. AF089094.1 GI:10503947
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Horikawa,Y. and Bell,G.I.
Direct Submission
Submitted (02-5EP-1998) Howard Hughes Medical Institute, The
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 2455)

Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del

Bosque-Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S., Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulze,J.,

Baler,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and
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                    1780 GAGGTGGAAGGACCAGGACCCCCACTGCTGCTGCAGGAGCCGCT 1829
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aLysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrV
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LOCUS AF089094
DEFINITION Homo sapiens ca
ACCESSION AF089094
VERSION AF089094 I GI:
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
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TITLE
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Percent Similarity: 99.257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17
AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysG1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCGGGCGGGCGGGGGGCGACGCCGGCGAGGGAGCTGTTCCGGGACGC 91
                                                     CTGGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWR RPQEICATPRLFPDDPREGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWAD OEVRGSFTCRIWQFGRWVEVTTDDRLFCLAGRLCFSCQREDVFMDPLLFRGGFWVLRA PVGRAGGGCPGGPDRRPGKWEPPERSRKRRPAGQARPLGAQDLSAAAPLEKGGFWVLRA LARQPQSRCPGAGGVPCLHCLGPAGAPGSGFVHPAAADPEPLGPAVLAGALERGG" 180 c 827 g 430 t
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1. .2455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="type F; alternatively spliced"
                                                 AAGGGTCCATGGGTCCTACGAGCACCTGTGGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 673
Gaps: 2
Percent Identity: 99.257
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467	450	434	417.	400	38 <b>4</b>	367	350	334	317	300	284	267	250	23 <b>4</b>	217	200	184
1430	1380	1330	1280	1230	1180	1130	1080	1030	980	930	880	830	780	730	680	630	580
euAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeu	aTyrAspArgGluValHisLeuArgCysGluLeuSerProGlyTyrTyrL	LeuProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAl	yrGlnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsn	lGlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisT	ArgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVa	heTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGln	nSerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysP	ArgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGl	alGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGlu	uPheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrV	ValaspalaalaValalaSerGluLeuLeuSerGlnLeuGlngluGlyGl	rgArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGlyGluGlyTrpSerGln	yGlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyA	LeuGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGl	lnCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGlu	oGlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspG	ArgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPr
483	467	450	433	417	400	383	367	350 <sup>-</sup>	333	317	300	283	267	250	233	217	<b>200</b>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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Ratio: 5.245
Harity: 96.131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                           COMMENT
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1 (bases 1 to 2602)
1 Hashimoto, K., Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirai, M., Terao, K. and Sugano, S.
Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB072744 2602 bp mRNA linear PRI 11-OCT-2001 Macaca fascicularis testis cDNA clone:QtsA-15844, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases I to 2602)
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (09-OCT-2001) Katsuyuki Hashimoto, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo capping; fis (full insert sequence).
Macaca fascicularis adult male testis cDNA to mRNA,
clone_lib:macaque testis cDNA library QtsA clone:QtsA-15844
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                    1530 CANGARCACCCCCGGGCACCTGCCTGCGGGGAGTGGGGGACTGGGGACCG 1579
                                                                                                                                                            1679
                                                                                                                                                                                                                                                                                                                       1729
                                                                                                                                                                                                                                                                                                                                                                                                                        1480 CGAGTCTTCTCTACCGGGCGAGTCTCCCTTAGCGCCCATCAGGGCAGTGGC 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1930 ACAGAGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATC 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650
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                                                                                                                                        517 alGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerArg
                                                                                                                                                                                                                              600 uLeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysL
                                                                     500 aLysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrV
                                                                                                                                                                                                              534 AsnPheAlaSerTyrProThrAsnProCysPheProPheSerValProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617 euLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 ThrGluGlyAlaPheThrValThrIleAlaThrArgIleAspArgProSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB072744.1 GI:16041091
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LOCUS AB072744
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R. Sitel: Drail (CACCACGT)
R. Sitel: Drail (CACCACGT)
R. Sitel: Drail (CACCACGT)
Description: 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTT); double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments cd. Skb. The Sfil-digested PCR product was cloned into distinct Drail sites of PME185-FL3. XhoI sites just outside the Drail sites can be used to isolate the CDNA insert. Libraries were constructed by oligo-capping method (Sugano et al.,University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CGTCTGCTCTAAAAGCTGCG]; 3' end primer [CGACTGGACTGACACA]).
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SYEHLWAGQVADALVDLIGGLAERWSLKGVAGSGGQDRLGRWFRTCRQLIRLIKDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISCSVLSPRAGARELGEFHAPIVSDLRELQDOAGOŠILLLRYONPWGRRCWOGLWRE
GGEGWSQVDAAVTSELLSQLQBGEFWVEEEEFLREFDEITIGYPITEAGHLQSLYTEK
LLCHTRALPGAWVKGQSAGGCRNNSGFPSNPKFWLRVSEPSEVYIAVLQRSRLRAVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGRARALVGDSHTSWSPASIPGKHYQAVGLHLMKVEKRRVNLPRVLSTPPVAGTACHA
YDREVHLENGELSPGYLAVPSTFLKRDAGEFLLEVEYSFGKASLSAIRAYKNASPRAA
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PRDTEFHPIGFHIFQVPEGGRSQDAPPLLLQCPPLLSCVPHRYAQEVSQLCLLPPGTYR
                          1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
[Email: Mashi@nih, go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1181)
Lab host: Toplo
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="testis"
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                                                                                                                                                    PME18S-FL3 (Acc.No. AB009864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 2602
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·	334 rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 350 ::
	317 1GlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 334 :
	301 PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 317 
	284 alaspalaalaValalaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 300                    1037 TAGATGCAGCGGTAACGTCTGAGCTCCTGTCCCAGCTCCAGGAAGGGGAG 1086
1	267 9ArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerglnV 284
	251 GlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 267 
	234 euGlyGluPheH1sAlaPheIleValSerAspLeuArgGluLeuGlnGly 250 
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	117 yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134 
	101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117 
	84 ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp 100 
	67 nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84 

OSETGLUVALTYTIEALAVALLEUGING GAGTGAGGTGTACHTYTIEALAVALLEUGING GAGTGAGGTGTACHTYTICCTCTCCAG SPTrpAlaGlyArgAlaArgAlaLeuVa	634 hrGluGlyAlaPhe 	617 uLeuProAlaGly	601 LeuSerCysVall            1987 CTGAGCTGCGTG	584 luGlyGlyArgs               1937 AGGGTGGCAGGA	567 oSerAspThrGl            1887 CAGGGACACCGA	551 GlyProGlyPro              1837 GGCCTGGCCCC	534 snPheAlaSerT               1787 ACTTTGCCTCGT	517 lGlnLeuArgGl 	501 LysAsnThrThr       :::::: 1687 AAGAACGCCAGC	484 rgValPheSerThrGly/               1637 GAGTCTTCTACCGGGG	467 uAlaValProSe              1587 GGCTGTCCCCAG	451 TyraspargGlu 	434 euProArgValLes 	417 rGlnAlavalGl              1437 CCAGGCTGTGGG	401 GlyaspSerHisThr	384 rgSerArgLeuHis                1337 GATCAAGGCTGCGT	367 eTrpLeuArgVal: 	
Leugina	ThrValThrIleAlaThrArgIleAspArg 	ThrTyrLysValValProSerThrTy           CTACAGGGTCGTGCCCTCACCTAA	SArgTyrAlaGlnGluValSeı 	rGlnAspAlaProPr             CCAGGACGCGCCCCC	HisProIleGlyPheHisIlePheGlnV 	CysValargIleThrLeuHisGlnHisCy 	ProThrAsnProCysPheProPheSerV 	SerTrpArgValGlyGlnThrAlaGlyGly               TCTGGAGAGCCGGCCAGACGGCGGGGGG	yAlaAlaLeuProAlaGlyGluTy               AGCAGCCCTGCCTGCGGGGGAGTC	\rgValSerLeuSerA 	rThrPheLeuLysAspAlaProGlyGluPheI                    CACCTTCCTGAAGGACGCGCCAGGGGAGTTCC	)CysGluLeuSerPro             TGCGAGCTCTCACCO	uSerMetProProValAlaGlyThrAlaCy 	LeuHisLeuTrpLysValGluLysArgArg 	SerTrpSerProAlaSerIleProGly 	AlaAlaAspTrpAlaGlyArgAlaArgAl     :::               CAGTGGACTGGGCAGGCCGGGCCCGGGC	SerGluProSerGluValTyrIleAlaVal 	* CASCASSASSCISCOSSANCAACASCSSCIIICCCASCAACCC
	roser	A I A	87 I	roLe       CGCT	25 I	Argp :::  CAGC	ProG1	rArg 	ω — <	న=౬	euLeuA        TGCTCC	I Yr	Hisal   +   Cacgo	alasn       TCAAT	SHIST	uVa GGT	G1n CAG	11000

651 IleHisSerGlnGluMetLeuGlyGlnPheLeuGlnGluValSerValMe 667

Sep

Fri

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PAT 08-AUG-2001
                                                                                          linear
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                                                                                          DNA
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Horikawa,Y., Oda,N., Hanis,C.L., Be
Polynucleotides encoding calpain 10
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 667
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Gaps: 1 Percent Identity: 91.518 Length: Ratio: 5.350 Percent Similarity: 91.518 Align seg 1/1 to: AR153291 Quality: 3290.00 US-09-768-877-2 x AR153291 alignment\_block

from: 1

34 17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL

92 cecerreceseseseses consequentes and second second 141 20 34 euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys

191

291 84 

367

101

342

1141 1041 1091 200 aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 184 641 217 691 234 741 250 791 267 841 891 300 317 991 334 320 367 284 941 alAspAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 1092 TCAGCAGGAGGCTGCCGGAACAACGGCCTTTCCCAGCAACCCCAAATT GlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 317 lGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 492 151 234 742 167 217 692 267 842 284 892 942 992 334 351 251 301

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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                           IleHisSerGlnGluMetLeuGlyGlnPheLeuGlnGluValSerValMe 667
                                                                                                                                                                                                                                                                                                                                                                                tAlaValMetLysThr 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgPr 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAGTGATGAAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTGACACCGAGTTCCACCCCATCGGCTTCCATATCTTCCAGGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oSerAspThrGluPheHisProIleGlyPheHisIlePheGlnValProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysLe 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGACCGGGAGGTCCACCTGCGTTGTGAGCTCTCACCGGGCTACTACCT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCCTGGCCCCGCTGCGTCCGCATCACTCTGCATCAGCACTGCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerArgA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgValPheSerThrGlyArgValSerLeuSerAlaIleArgAlaValAla 500
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 Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinoklo,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del Bosque-Platta,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S., Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulze,J., Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and
                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2297)

1 (bases 1 to 2297)
                                                                                                                                                                                                                                            AFUB9090 2297 bp mRNA
Homo sapiens calpain-like protease CAPN10b
                                                                                                                                                                                                                AF089090.1
                                                                                                                                                                                                                GI:10503938
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JOURNAL
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AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl
                                                        ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp 100
                                                                                                                               nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL
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                                                                                                                                                                                                                                                                                                                               TGGCCCAGTTCCGCGAGGACATCACGTGGAGGCGGCCCCCAGGAGATTTGT
                                                                                                           GGGGCTGCTGGGGATTGCTGGTTCCTGTGTGCCTGCGCCGCGCTGCAGA
                                                                                                                                                                                  GCCACACCCCGGCTGTTTCCAGATGACCCACGGGAAGGGCAGGTGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-SEP-1998) Howard Hughes Medical Institute, The University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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: 5.350
: 91.518
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2289. .2294
713 c 772 g 408 t
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LLCHTRALFGAWVKGGSAGGCKNNSGFPSNPKFWLRVSEPSEVYLAVLQRSRLHAADW
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YDREVHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLRALAPAASASICIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPQEICATPRLFPDDPREGOVKOGLLGDCWFLCACAALOKSRHLLDQVIFPGOPSWAD
GEYRGSFTCRIWGFGRWEWTTDDRLFCLAGRLCFSRCQREDWFWLFLLEKVYARVHG
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LISCCYLSPRAGARELGEFHAFIVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWRE
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/db_xref="G1:10503939"
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/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="type B; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="2q37"
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1. .2297
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Gaps: 1
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341

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141

1242 GGTGACAGTCATACTTCGTGGAGCCCAGCGAGCATCCCGGGCAAGCACTA 1291

	417	GlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisTy	401
	400	rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaALeuVal 	384
	384 1191	eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 	
	367 1141	Seraladlydlydysargasnasordlyphebroserasnprolysph 	50 00
	350 1091	rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 	ო. ▼
	334	lGlyfyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 	317 992
	317 991	PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 	301
٠.	300	alAspalaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 	284
	284	gargCysTrpGlnGlyLeuTrpargGluGlyGlyGlyGlyTrpSerGlnV 	267
	267	GlnaladlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 	251 792
	250	euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 	234
	234	ncysLeulleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL 	217 692
	217 691	. GlyargtrpGluHisargThrCysargGlnLeuLeuHisLeuLysaspGl 	201
	200	rgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPro	184 592
	184	aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 	167 542
	167	. LeuglulysvalfyralalysvalHisGlySerfyrgluHisLeufrpal 	151
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	391		34.

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43,	4 euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450 
45. 1392	1 TyraspargGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe 467 
467	7 ualaValProSerThrPheLeuLysAspalaProdlyGluPheLeuLeuA 484 
484	<b>**</b> 0
501	LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa 517
1523	2
517	lGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGly
1523	2
534	4 snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu 550
1523	2 1522
55]	1 GlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgPr 567 
567 1573	7 oSerAspThrGluPheHisProIleGlyPheHisIlePheGlnValProG 584 
584 1623	4 luGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGlnGluProLeu 600 
601	1 LeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysLe 617 
617	7 uLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAspT 634 
634	4 hrGluGlyalaPheThrValThrIlealaThrArglleAspArgProSer 650 
651	IleHisSerGinGluMetLeuGlyGlnPheLeuGlnGluValSerValWe 667 
66 <b>7</b> 1873	talavalMetLysThr 672 
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seq_docu LOCUS DEFINITI ACCESSIC VERSION	seq_documentation_block: LOCUS AR153294 LOCUS AR153294 AR153294 ACCESSION AR153294 AR153294.1 GI:15120826

KEYWORDS SOURCE ORGANISM ORGANISM TITLE JOURNAL JOURNAL FEATURES SOURC BASE COUNT ORIGIN	Unknown.  M Unknown.  Unclassified.  1 (bases 1 tc.  Horikawa,Y., C  Polynuclectide  Patent: US 623  Patent: US 623  Patent: US 623  1 . 2  /orga  1 . 2  scores:
ercent	similarity: 82.550 Percent Identity: 82.416
alignment US-09-76	58-877-2 x AR153294
Align se	9 1/1 to: AR153294 f
. 42	MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17 
17	aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
. 92	
34	euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys 50
142	
51	AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl 67
192	
67	nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84
242	
84	ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp 100
292	
101	AlaAspGlnGluTyrArgGlySerpheThrCysArgIleTrpGlnPheGl 117
342	
117	yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134
392	
134	rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
442	
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492	
167	aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 184
542	
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592	

_	154	1492 TGTCTGGGACAGATACTGGCGCCAGGGCCAAGTGAAGCCCCGGGATTGGTA	
	427	– pı`	
ŭ	149	1442 GGGCCACGGTGCCTTTGTGGGCCCAGCTACAAGGAGGACTTGCAGGCTCG	
•	426	426	
ï	144	1392 GCAAAAGAAGTTGCTGGAAGGCCCCACTGTCCAGCAGCCCCCCAGGTTGCCT	
•	426	426	
1	139	1342 TGTTCCCTGTCCCTTCATGGATGTGGCCCACATGATGTTCCTTTTCCTCTT	
Ŭ,	426	426	
Ξ ,	426 134	417 rGlnAlaValGlyLeuHisLeuTrpLys	
)	417 129	401 GlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysH1sTy	
1 0	400 124	384 rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 	
1 -	384 119	367 eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 	
11	367 114	351 SeralaGiyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh	
9 0	350 109	334 rgLeuLeuCysH1sThrArgAlaLeuProGlyAlaTrpValLysGlyGln 	
<u> </u>	334 104	317 1G1yTyrProValfhrGluAlaG1yHisLeuGInSerLeuTyrThrGluA 	
1 7	317 991	301 PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 	
ъ 6.	300 941	284 alaspalaalaValalaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 	
	284 891	267 9ArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnV 	
7	261 841	251 GlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 	
р 0	250 791	234 euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 	
д д	234 741	217 nCysLeulleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL 	
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428 GluLysArgArgValAsnLeuProArgValLeuSerMetProProValAl 444

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Hinokio, Y., Lindner, T.H., Mashima, H.
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Ratio: 5.267
Harity: 82.550
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TITLE
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Locus Ar089093 2516 bp mRNA linear PRI 23-JAN-2001
DEFINITION Homo sapiens calpain-like protease CAPN10e mRNA, complete cds.
ACCESSION AP089093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2516)
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                                                                                                      528 ThralaGlyGlySerArgAsnPheAlaSerTyrProThrAsnProCysPh 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euHisGlnHisCysArgProSerAspThrGluPheHisProIleGlyPhe 577
                                                           544 eProPheSerValProGluGlyProGlyProArgCysValArglleThrL
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Location/Qualifiers

1. 2516
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ Chromosome="2"
/ Map="2437"
/ Ap. 1376
/ Ap. 1379
/ Ap. 1376
/ Ap. 137
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AGRARALVGDSHTSWSPASIPGKHYQAVGLHLWKGVTLGTTLFPVPSWMWPT"
Bosque-Plata, L., Horikawa, Y., Oda, Y., Yoshwarz, P.E., del
Bosque-Plata, L., Horikawa, Y., Oda, Y., Yoshluchi, I., Colllla, S.,
Polonsky, K.S., Wei, S., Concannon, P., Iwasaki, N., Schulze, J.,
Ball, G.I.
Genetic variation in the gene encoding calpain-10 is associated
with type 2 diabetes mellitus
Nat. Genet. 26 (2), 163-175 (2000)
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Gaps: 2
Percent Identity: 82.416
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400 1241	rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal	·384 1192
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1191		1142
367	SeralaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh	351
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350	1 rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln	334
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991		942
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941		892
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891		842
267	1 GinālaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr	251
841		792
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791		742
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741		692
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691		642
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184	7 aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA	167
591		542
167 541	1 LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl 	<b>ن</b> ف
150 <b>49</b> 1	4 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 	Aυ
134	7 yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA	117
441		397
117	1 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl	10:
391		34:

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1741 ...... 1741

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	527	laGlyGluTrpGlyThrValGlnLeuArgGlySerTrpArgValGlyGln	511
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	<b>477</b> 1691	euSerProGlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAla 	461 1642
	461 1641	aGlyThrAlaCysHisAlaTyrAspArgGluValHisLeuArgCysGluL 	444 1592
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491

200 641 217

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234 741 250

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Unknown,

SOURCE ORGANISM

DEFINITION ACCESSION VERSION KEYWORDS 267

841

791

284

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941 317 991 334

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1973 TCCACCTACCTGCCGGACACAGGGGGGCCTTCACAGTGACCATCGCAAC

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                                                                                                                                                                                                              and Cox, N.J.
        661
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                2023 CAGGATTGACAGGCCATCACAGCCAGGAGATGCTGGGCCAGTTCC
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                                                                                                                                                                               Unclassified.
Unclassified.
1 (bases 1 to 2204)
1 (bases 1 to 2204)
2 Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I. and Polynucleotides encoding calpain 10
L Patent: US 6235481-A 9 22-MAY-2001;
1 Location/Qualifiers
1. 2204
1. 2204
                                                                                                                                                                                                                                                                                                                           Length: 672
Gaps: 1
Percent Identity: 86.905
                                           to: 2204
                                                                                                                Sequence 9 from patent US 6235481.
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Ratio: 5.292
Percent Similarity: 86.905
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LOCUS AR153293
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alignment\_scores

source

TITLE JOURNAL REFERENCE AUTHORS

FEATURES

BASE COUNT

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384

400

417

101 342 1341

associated

Chicago, The

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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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LOCUS AF089092
                REFERENCE
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   Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2204)
                                                                                                                                      Homo sapiens calpain-like protease CAPN10d AF089092
                                                                                                                    AF089092.1 GI:10503943
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                                                                                                                                                                 PRI 23-JAN-2001
                                                                                                                                                   cds.
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US-09-768-877-2 x AF089092
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AF089092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                142
                                                                                                             192
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                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                            42 ATGCGGGCCGGGGCGCGACGCCGACGCGAGGGAGCTGTTCCGGGACGC
                                                                                                                                                                                                                                                                                                                                       1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl
                                GCCACACCCCGGCTGTTTCCAGATGACCCACGGGAAGGGCAGGTGAAGCA
                                                                                                                        AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl
ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 3090.50
Ratio: 5.292
milarity: 86.905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-SEP-1998) Howard Hughes Medical Institute, University of Chicago, 5841 S. Maryland Avenue, MC1028,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic variation in the gene encoding calpain-10 is with type 2 diabetes mellitus
Nat. Genet. 26 (2), 163-175 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinoklo,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del Bosque-Platta,L., Horikawa,Y., Oda,Y., Toshiuchi,I., Colilla,S., Polonsky,K.S., Wei,S., Concannon,P., Twasaki,N., Schulze,J., Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikawa, Y. and Bell, G.I. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bell,G.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20472315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGRARALUGDSHTSWSPASIPGKHYQAVGLHLMKVEKRRVNLPRVLSMPPVAGTACHA
YDREVHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLRSQRVEGARTHPHCC
CRSRC*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="calpain-like protease CAPN10d"
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SYEHLWAGGVADALVDLTGGLAERWHLKGVAGSGGQDRPGGWEHRTCRQLLHIKDQC
SYEHLWAGGVADALVDLTGGLAERWHLKGVAGSGGQDRPGTWEHRTCRQLLHIKDQC
LISCCVLSPRAGARELGEFHAFIVSDLRELGGQAGQCILLLRIQNPWGRRCWGGLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEGWSQVDAAVASELLSQLQEGEFWVEEEEFLREFDELTVGYPVTEAGHLQSLYTER
LLCHTRALFGAWVKGQSAGGCRNNSGFPSNPKFWLRVSEPSEVYIAVLQRSRLHAADW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12. .1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="type D; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'map="2q37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       672 c
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67

191

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241

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91

1192 GATCCAGGCTGCACGCGGGGGGCTGGGCCGGGCCCGGGCCACTGGTG 1241

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  G 341	eGl 117       TGG 391	yA 134    GA 441	eu 150    TA 491	Al 167    GC 541	lua 184     '     '	Pro 200      CCA 641	G1 217     CA 691	luL 234      AGC 741	1y 250      791	Ar 267     CG 841	nV 284       G 891	lu 300       941	Va 317    3T 991	uA 334  -   GA 1041	Gln 350     CAG 1091	Ph 367    TT:1141	nA 384     GA 1191	al 400 
CAGCCGAGCT	eTrpGlnPh            TTGGCAGTT	ysLeuAlaGl              GCCTTGCAGG	eTrpLeuProL	uHisLeuTrp            GCACCTGTGG	lyLeualag             GCCTGGCAG	Asparg	3=5	Alaarggl            scccggga	3luLeuGlnGl 	ProTrpGly 	yTrpSerGl	slnGluGlyGli 	AspGluLeuThrV	CLeuTyrThrGlu 	alLysGly            TCAAGGGC	AsnProLys                AACCCCAAA	aValLeuGl              GTCCTGCA	rgAlaLeuV.
TCCTCCGGGACAC	SerPheThrCysargIl 	ArgLeuProC	alPh      TGTT	lyserfyrgl 	LeuThrGlyG 	rGlyGlyGlnGln 	InleuLeuH1	SerProArgAlaGly/                      \GCCCCAGAGCAGGT	rAspLeuArg               GACCTGCGG	uLeuLeuArgIleGlnAsn) 	luGlyGlyGluGl 	euSerGinLeuGind 	gGluPhe 	euGlnSerLe                  TGCAGAGCCT	oGlyAlaTrpV                 TGGGCCTGGG	yPheProSe	alTyrileal 	Glyargalaa !!!!!!!!
ACCAGGTCAT	61y 	GluvalThrThrAspAspArgLeup 	gCysGlnArgGluAspV 	ralaLysValHisGlySerTyr 	laAspAlaLeuValAspLeuThrGly  }	alalaglyse: 	ThrCysArgG.	/alleus          srgcrcz	nelleValse 	eLeuLeuLeuAı 	parge         Gagag	rGluLeuLer 	luPheLeuAr	AlaGlyHisi 	laLeuPr 	AsnAsnSerG1                   AACAACAGCGG	luProSerGluVa 	aAspTrpAla
	aAspGlnGluTyrArg( 	급드입	PheserAr           TTCTCCCG	SValTy           GTCTA	<b>≤</b> = %	AsnLeuLysGlyvalalaGlySerG 	ArgrrpGluHisArgThrCysArgGlnLeuLeuHis 	leSerCysCys\                 CAGCTGCTGC	GlupheHisalaPheIleValSerAspLeuArgGluLeuG 	InCysIl 	rpGlnGlyLeuTr 	AspalaAlavalAlaSerGluLeuLe 	PherrpvalGluGluGlubhereuard 	GlytyrprovalthrGlualaglyhisteuginser 	CysHisThrargA 	yGlyCysArgA                   AGGCTGCCGGA	rgValSerGlu 	LeuHisAlaAl 
	A16	yArgTrpV            ACGCTGGG	rgLeuCys          GACTCTGT	LeuGluLy          CTGGAAAA	aGlyGlnVal	rgTrp        GATGG	61y     660	nCysLeulleSer 	euGly        TGGG	GlnAlaGlyG] 	gArgCysT           GCGGTGCT	4 FI	-	- E	rgLeuLeuC 	SerAlaGly             TCAGCAGGA	eTrpLeuAr 	rgSerArgi
29.	342	392	134	151	167	184	201	217	234	251 792	267	284	301	317 992	334	351 1092	367 1142	384

401	GlyaspserHisThrSerTrpSerProAlaSerIleProGlyLysHisTy 417 
417	rGlnalaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL 434
434	eubroargyalLeuŝerMetProProPalalaGlyThralaCysHisAla 450 
451	TyraspargluvalHisLeuargCysGluLeuSerProGlyTyrTyrLe 467 
467	uAlaValProSerThrPheLeuLy 
484	rgvalP        GAGTCT
501	LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrV
1522	
. 517	lGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerAr
1522	
534	snPheAlaSerTyrProThrAsnProCysPheProPheSerValProG
1522	
551	GlyProGlyProArgCysValArgIleThrLeuH1sGlnH1sCysArg
1522	1522
267	oSerAspThrGluPheHisProlleGlyPheHisIlePheGlnValPr
1523	
584	luGlyGlyArgSerGlnAspAlabroProLeuLeuGlu 
60 <b>1</b> 1580	LeuSerCysValProHisArgTyrAlaglnGluValSerArgLeuCysLe 617 
617	erfhrfyrLeuProA 
634	hrGluGlyAlaPheThrValThrIlealaThrArgIleAspArgFroSer 650 
651	TIEHISSErGInGluWetLeuGlyGlnPheLeuGlnGluValSerValMe 667
667 1780	talavalmetiysThr 672 
sed_name	: gb_ro:BC010969 · · ·
sea docum	mentation block.

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BASE COUNT
ORIGIN
alignment_block:
US-09-768-877-2 x BC010969
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                                                                                                Percent Similarity:
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JOURNAL
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                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: 1 Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753259. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Mus musculus,
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                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="calpain 10"
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                                                                                                2969.00
4.758
92.996
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HPIGFHVFQVPADGENDACISLLQEPLLSCVPHRYAQEVSRLCLLSVGNYRIVPSTY
LPDYEGTFTVTIATRIDRQSIHSQEMLGQLLQEVSFMAVMKA*
1 713 c 749 g 529 t
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/clone="MGC:13731 IMAGE:4159612"
/tissue_type="Liver, normal. 5 mc
/clone_lib="NCI_GGAP_Li9"
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/db_xref="LocusID:23830"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2528 bp mRNA linear ROD: calpain 10, clone MGC:13731 IMAGE:4159612,
                                                                                                    Percent
                                                                                                Identity: 81.222
                                                                                                                                                                Length:
                                                                                                                                                                671
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, mRNA,
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911
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                                                                                                                                                                                                                                                                                                                                                                                            511
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euGlyGluPheH1sAlaPheIleValSerAspLeuArgGluLeuGlnGly
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|TCGGAGAGTTCCATGCCTTCATCATCTCAGATCTGCAGGAGCTCAGGAGT
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                                          ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp
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- PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa
- - rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 350
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Sequences:

Sequences:

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Search time (sec): 278.420000
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                               15-AUG-2000 (first entry)
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7 7.2e-1
8 9.1e-1
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NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; calpain 10a; diapain-1; cysteine protease; chromosome 2; human; diagnosis; therapy; ss. Location/Qualifiers 178..2196

98US-0105052 99US-0134175 99WO-US24890

DEV CORP.

Horikawa ۲ 0da ž Sreenan Ś Zhou ۲, Otani 7

Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -

Claim 65; Page 219-220; 257pp; English.

The present sequence is that of cDNA corresponding to the major transcript of the human calpain 10 gene, CAPNIO (see AAZ27475), carciuding the polyA tract. The sequence contains an open reading frame that encodes a protein of 672 amino acids (see AAY79567), designated calpain 10a. The CAPNIO gene consists of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10h, respectively. Isoform 10a is encoded by exons 1-7 and 9-13 of the CAPNIO gene. Transcripts encoding calpain 10a are the most abundant in the various tissues examined. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A G-to-A polymorphism in intron 3 of the CAPNIO gene in the NIDDMI region of chromosome 2 (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based on detection of a polymorphism in a calpain encoding nucleic acid, especially UCSNR-10 of the CAPNIO gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin

T; 0 other mediated glucose BP; 448 A; 819 C; 899 G; 454 insulin ö Sequence 2620 alignment\_scores 2 × 3

Length: 672 Gaps: 0 Percent Identity: 100.000 Quality: 3649.00 Ratio: 5.430 Percent Similarity: 100.000 alignment\_block: US-09-768-877-2 x AAA27476

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10-AUG-1998;
                        06-AUG-1999;
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                                                                          W0200009709-A2
                                                                                                                          misc_binding
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                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                       Protease and associated protein-13; PPRG-13; anti-PPRG antibody; diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic; hepatototropic; antiinflammatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic;
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98US-0096114
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1784..1831
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REAL SECTION OF THE S
                                                                                                                                                                                derived from OVARNOTO? cDNA library. It encodes human protease and associated protein-13 (PPRG-13), which is expressed in nervous and reproductive tissues. Anti-PPRG antibodies can be used as therapeutic antagonists, reagents for diagnosis and monitoring diseases and for isolating PPRG. PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring of PPRG-PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring of PPRG-PPRG diseases and gene mapping. PPRG can be used in the treatment of cell proliferative disorders like cancer, arteriosclerosis, atherosclerosis, bursitts, cirrhosis and hepatitis, and immune disorders like AIDS, Addison's disease, adult respiratory distress syndrome, allergies, and provincing and province and
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Corley NC,
Sequence 2594 BP; 450 A; 812 C; 884 G; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a cDNA identified in Incyte clone 1902576 derived from OVARNOTO7 cDNA library. It encodes human protease and
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P-PSDB; AAY70019.
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YT, Reddy R,
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n C, Au-Young
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alignment\_scores: Quality: Ratio: alignment\_block: US-09-768-877-2 x AAZ50930 Align seg 1/1 to: Percent Similarity: AAZ50930 5.423 100.000 3644.00 Percent Identity: 99.851 Length: 672

149 ATGCGGGCGGGCGGGGGGGCGACGCGAGGGAGCTGTTCCGGGACGC 1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl from: 1 to: 34 198

199 17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL CGCCTTCCCCGCCGCGGACTCCTCGCCTCTTCTGCGACTTGTCTACGCCGC 248

117 YARGTIPValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134

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                                                                                                                                            1GlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA
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                             luGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGlnGluBroLeu
                                                                                                                                                                                                                                                                                                      AGGGTGGAAGGAGCCAGGACGCACCCCCACTGCTGCAGGAGCCGCTG
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euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla
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ID AAK94261 standard;
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alignment_block:
US-09-768-877-2 x AAK94261
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Ratio: 5.414
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAK94261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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11-JAN-2000;
02-MAY-2000;
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      YSSerArgH1sLeuLeuAspGlnValIleProProGlyGlnProSerTrp
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2000JP-0118774.
2000JP-0183765.
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Gaps: 0
Percent Identity: 99.702
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rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 400
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SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh
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                                                                   euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA27481

GGCAGTGATGAAAACC 2163

2148

seq\_documentation\_block:
ID AAA27481 standard; cDNA; 2455 BP

The present sequence is that of cDNA corresponding to a minor transcript of the human calpain 10 gene, CAPN10 (see AAZ7475).

The sequence contains an open reading frame that encodes a protein of 174 amino acids (see AAY79572), designated calpain 10f. The capus of 15 exons spanning 32 kb. A complex pattern of 274 amino acids (see AAY79572), designated calpain 10f. The capus of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10b, respectively. Calpain 10f is encoded by exons identification of genes responsible for type 2 diabetes for use in clasmostic and therapeutic applications. A G-to-A polymorphism in clasmostic and therapeutic applications. A G-to-A polymorphism in clasmost of the CAPN10 gene in the NIDDM1 region of chromosome 2 (UCSNP-43) shows evidence for linkage to type 2 diabetes are methods for screening for a propensity for type 2 diabetes are methods for screening for a propensity for type 2 diabetes are also cald, especially UCSNP-10 of the CAPN10 gene. Methods are also cald, especially UCSNP-10 of the CAPN10 gene. Methods are also cald, especially UCSNP-10 of the CAPN10 gene. Methods are also didentifying modulators of calpain activity using calpain 10 cencoding polynucleotides, including the present sequence; dentifying modulators of calpain activity using calpain 10 centors and activity using calpain 10 centors activity using calpain 10 centors and activity using calpain 10 centors and activity using calpain 10 centors activit Zhou Y, Otani K; Method for screening for type 2 diabetes mellitus comprises of polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment. polypeptides and nucleic acids, and using these modulators treat diabetes, in particular through the regulation of an NIDDM1; non-insulin-dependent diabetes mellitus; CAPNIO calpain 10; calpain 10f; diapain-1; cysteine protease; chromosome 2; human; diagnosis; therapy; ss. secretory response or insulin mediated glucose transport. Oda N, Sreenan S, Claim 65; Page 232-232; 257pp; English Location/Qualifiers 42..866 /\*tag= a 99WO-US24890. 98US-0105052. 15-AUG-2000 (first entry) Horikawa Y, Human calpain 10f cDNA (ARCH-) ARCH DEV CORP WPI; 2000-339702/29. Hanis CL, Bell GI; P-PSDB; AAY79572. WO200023603-A2 Homo sapiens 21-OCT-1998; 13-MAY-1999; 21-OCT-1999; Polonsky KS, 27-APR-2000 Key 

Sequence 2455 BP; 429 A; 769 C; 827 G; 430 T; 0 other;

alignment\_scores:
Quality: 3604.00 Length: 673
Ratio: 5.395 Gaps: 2
Percent Similarity: 99.257 Percent Identity: 99.257

alignment\_block: US-09-768-877-2 x AAA27481

7 rgArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTr 	LeuGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnG1 25	4 N O N	167 laGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGlu 183	134 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150 .	101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheG1 117	67 nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84	34 euAlaGinPheargGluAspIleThrTrpArgArgProGlnGluIleCys 50	GCGCGACGCCGAGGGAGCTGTTCCGGGA AASpSerSerLeuPheCysAspLeuSerThrF 	Align seg 1/1 to: AAA27481 from: 1 to: 2455 1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeupheArgAspAl 17 
ToSerAspThrGluPheHisProIleGlyPheHisIlePheGinValProIleGlyPheHisIlePheGinValProIleGlyPheHisIlePheGinValProIleGlyPheHisIleIl	AlaSerTyrProThrAsnProCysPheProPheSerValProG1 	500 aLysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrV 517	467 euAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeu 483	434 LeuProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAl 450	400 lGlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisT 417	367 heTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGln 383	334 ArgLeuleuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGl 350	7 alGly 11111 0. TIGGO	00

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Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otani K;
                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA27477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIDDM1; non-insulin-dependent diabetes mellitus; CAPNIO gene; calpain 10; calpain 10b; diapain-1; cysteine protease; chromosome 2; human; diagnosis; therapy; ss.
                                                          1980 CATTCACAGCCAGGAGATGCTGGGCCAGTTCCTCCAAGAGGTCTCCGTCA 2029
                             1830 GCTGAGCTGCGTGCCACATCGCTACGCCCAGGAGGTGAGCCGGCTCTGCC 1879
                                                                                                                                         1930 ACAGAGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATC 1979
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                                                                                                                         634 ThrGluGlyAlaPheThrValThrIleAlaThrArgIleAspArgProSe
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42..1676
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ID AAA27477 standard; cDNA; 2297
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P-PSDB; AAY79568.
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many tissues, including skeletal muscle and islets. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A c-to-A polymorphism in intron 3 of the CAPNIO gene in the NIDDMI region of chromosome 2 (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes are based on detection of a polymorphism in a calpain conding nucleic acid, especially UCSNP-10 of the CAPNIO gene. Methods are also claimed for producing calpain 10 polypeptides wising calpain 10-encoding polymorlectides, including the present sequence: identifying modulators of calpain activity using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.
    It is readily detectable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 CGCCTTCCCCGCCGCGGGACTCCTCGCCTCTTCTGCGACTTGTCTACGCGC 141
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                                                                                                                                                                                                                                                                                                               Sequence 2297 BP; 404 A; 713 C; 772 G; 408 T; 0 other;
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Percent Identity: 91.518
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Ratio: 5.350
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                 TACGACCGGGAGGTCCACCTGCGTTGTGAGCTCTCACCGGGCTACTACCT 1441
                                                               TyrAspArgGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe 467
                                                                                                  euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450
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                           ATTCACAGCCAGGAGATGCTGGGCCAGTTCCTCCAAGAGGTCTCCGTCAT 1872
                                   | IleHisSerGlnGluMetLeuGlyGlnPhéLeuGlnGluValSerValMe
                                                          CAGAGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATCC
                                                                  hrGluGlyAlaPheThrValThrIleAlaThrArgIleAspArgProSer
                                                                                                                                                snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu
                                                                                                                                                                                                                                                                                                                                 lGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerArgA 534
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seq\_documentation\_block:
ID AAA27480 standard: seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA27480

AAA27480 standard; cDNA; 2516

ВP

15-AUG-2000 (first entry)

Human calpain 10e cDNA.

NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 calpain 10; calpain 10e; diapain-1; cysteine protease; chromosome 2; human; diagnosis; therapy; ss.

Homo sapiens

Key CDS

/\*tag=

Location/Qualifiers

WO200023603-A2

27-APR-2000

21-OCT-1999; 99WO-US24890

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Zhou Y,

Sreenan S,

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Horikawa Y,

98US-0105052. 99US-0134175.

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The present sequence is that of cDNA corresponding to a minor transcript of the human calpain 10 gene, CAPN10 (see AA27475).
The sequence contains an open reading frame that encodes a protein of 444 amino acids (see AAY9571), designated calpain 10e. The calpain splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY99567-74), designated calpain 10a to 10h, respectively. Calpain 10e is encoded by exons calpain 10a to 10h, respectively. Calpain 10e is encoded by exons 110* and 11:13 of the gene. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A G-to-A polymorphism in clark of the CAPN10 gene in the NIDDMI region of chromosome 2 (UCSNP-43) shows evidence for linkage to type 2 diabetes are methods for screening for a propensity for type 2 diabetes are concerned on detection of a polymorphism in a calpain encoding nucleic acid, especially UCSNP-10 of the CAPN10 gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10 polypeptides using calpain 10 polypeptides and nucleic acids; and using the present sequence; identifying modulators of calpain activity using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.
                                                                                                                                                                                                                                                                   Method for screening for type 2 diabetes mellitus comprises polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -
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                                                                                        (ARCH-) ARCH DEV CORP
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P-PSDB; AAY79571.
                                                                                                                                                        Bell GI;
                                            13-MAY-1999;
                                                                                                                                   Polonsky KS,
                     21-0CT-1998;
                                                                                                                                                            Hanis CL,
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Sequence 2516 BP; 445 A; 777 C; 837 G; 457 T; 0 other;

Length: 745 Gaps: 2 Percent Identity: 82.416 Ratio: 5.267 Percent Similarity: 82.550 Quality: 3239.50 alignment\_scores: alignment\_block:

US-09-768-877-2 x AAA27480

from: 1 to: 2516 Align seg 1/1 to: AAA27480

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- 67 51 AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl

191

1041 1091 YARGTIPVAlGLUVAlThITHIASPASPARGLEUPTOCYSLEUALAGLYA 134 117 391 167 541 184 200 641 217 691 234 741 250 267 841 284 300 941 317 350 791 891 991 334 367 384 CTGGAAAAGGTCTACGCCAAGGTCCATGGGTCCTACGAGCACCTGTGGGC rgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPro ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA nCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL 284 alAspAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu GlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspGl 301 PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 1092 TCAGCAGGAGGCTGCCGGAACAACAGCGGCTTTCCCAGCAACCCCAAATT eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 101 342 117 392 151 492 167 542 184 592 842 201 217 267 351 1142 367

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DT 15-AUG-2000 in 10d cDN
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WIDDM1; non-insulin-d
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KW NIDDM1; non-insulin-d
KW calpafn 10; calpain 1
KW calpafn 2; human;
XX
OS Homo sapiens.
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Thus The AAA27479;
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Thus AAA27479; calpain 2
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Thus AAA27479; calpain 3
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA27479
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Hanis CL, Bell GI;
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13-MAY-1999;
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The present sequence is that of cDNA corresponding to a minor transcript of the human calpain 10 gene, CAPN10 (see AAZ27475).

The sequence contains an open reading frame that encodes a protein of 513 amino acids (see AAX79570), designated calpain 10d. The CAPN10 gene consists of 15 exons spanning 32 kb. A complex pattern conflict a splicing generates proteins of 672, 544, 517, 513, conflict and the splicing generates proteins of 672, 544, 517, 513, conflict and the splicing acids (see AAX79567-74), designated calpain 10a to 10h, respectively. Calpain 10d is encoded by exons conflict and 11-13 of the gene. The invention concerns the dentification of genes responsible for type 2 diabetes for use in chargonstic and therapeutic applications. A G-to-A polymorphism in control of the CAPN10 gene in the NIDDM1 region of chromosome 2 (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed contents are

Claim 65; Page 227; 257pp; English.

based on detection of a polymorphism in a calpain encoding nucleic acid, especially UCSNP-10 of the CAPN10 gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polymucleotides, including the present sequence; identifying modulators of calpain activity using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.

752 G; 390 T; 0 other; Sequence 2204 BP; 390 A; 672 C;

Percent Identity: 86.905 to: 2204 from: 1 Ouality: 3090.50 Ratio: 5.292 Percent Similarity: 86.905 Align seg 1/1 to: AAA27479 alignment\_block: US-09-768-877-2 x AAA27479 alignment\_scores

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nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84 242 GGGGCTGCTGGGGGATTGCTGGTTCCTGTGTGCCTGCGCCGCGCTGCAGA

101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl

yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 

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GlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 792 CAGGCGGCCAGTGCATCCTGCTGCGGATCCAGAACCCCTGGGGCCG 301 PheTrpValGluGluGluPheLeuArgCluPheAspGluLeuThrVa nCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 1392 TACGACCGGCAGGTCCACCTGCGTTGTGAGCTCTCACCGGCCTACTACCT rGlnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla TyrAspArgGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe uAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuA rgValPheSerThrGlyArgValSerLeuSerAlaIleArgAlaValAla LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa GAGTCTTCTCTACCGGGCGAGTCTCCCTTAG 

snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu

1522

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AC AAA27484;
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DT 15-AUG-2000 (first e
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DT 10 gene
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Calpain 10; diapain-1
KW calpain 10; diapain-1
KW diagnosis; therapy; s
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Calpain 10; diapain-1
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PD 27-APR-2000.
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PP 21-OCT-1999; 99WO-U
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PF 21-OCT-1998; 98US-C
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PR 13-MAY-1999; 99US-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCACAGCCAGGAGATGCTGGGCCAGTTCCTCCAAGAGGTCTCCGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA27484
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
    Horikawa Y,
                                                           98US-0105052.
99US-0134175.
                                                                                                      99WO-US24890
                                                                                                                                                                                                         Location/Qualifiers
                                 CORP
                                                                                                                                                                                                                                                                                                                                           gene.
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 Sreenan S;
zhou Y,
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Otani K;
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The present sequence corresponds to the major transcript of the course CARNIO gene encoding calpain 10 (see AAY79575), a novel cysteine protease. Calpain is ubiquitously expressed in mouse and the cysteine protease. Calpain is ubiquitously expressed in mouse and chumans. The invention concerns the identification of genes cresponsible for type 2 diabetes for use in diagnostic and therapeutic applications. A polymorphism in intron 3 of the human characteristic capplications. A polymorphism in intron 3 of the human characteristic capplications. A polymorphism in a calpain capped to the capped the concerns the polymorphism in a calpain cencoding nucleic acid. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polynucleotides, calpain 10 polypeptides using calpain 10-encoding modulators of calpain cactivity using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated
                                                                                                                                                                                                                                                                                                                                                                                                                      glucose transport.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 65; Page 236-237; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanis
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DB; AAY79575, AJ
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alignment\_scores: Percent Similarity: Quality: Ratio: : 2963.00 4.756 92.846 Gaps: 2
Percent Identity: 81.073 671 2

Sequence 2511 Bp; 523

Α,

708

Ç 749

G; 531 T;

0 other;

alignment\_block: US-09-768-877-2 x AAA27484

Align seg 1/1 to: AAA27484 from: . 6

50 258 67	34 eualaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys 50	34 209 51
34	17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34	17 159
158	ATGCGGGCGGTCCGGGCCGAGACGCCGGCGCGGAGCTCTTCCGGGACGC	109
17		_

409

359

ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp |||||:::|||||||||||||||||:::|||| | AGAGTCAACACCTCCTGGACCAGGTCTTCCCTCCAGGACAGCCAGGCTGG

408 100 358

84

101

309

Fri

134	rgleuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 1 	50
151 559	LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl 1 	67
167	aGlyGlnValalaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 1: 	84 58
184 659	rgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlyGlnGlnAspArgPro 2.	00
201	rCysArgGlnLeuLeuHisLeuLysAspGl 2 	17
217	nCysLeulleSerCysCysValLeuSerProArgalaGlyalaArgGluL 2:	34
234	euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 2: 	50
251 859	GlnalaGlyGlnCysIleLeuLeuLarglleGlnasnProTrpGlyar 2/     :::	67
267	9ArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnV 20 	84 5.8
284	alaspalaalayalalaserGluLeuLeuSerGlnLeuGlnGluGlyGlu 3(	00
301 1009	PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 3:	17
317 1059	GlyTyrProValThrGlualaGlyHisLeuGlnSerLeuTyrThrGlua 3: 	34
334	rgLeuLeuCysHisThrArgAlaLeuProGlýAlaTrpValLysGlyGln 35   -::	50 158
351 1159	SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 36	67 208
367 1209	eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 36 	84 258
384 1259	rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 4(	299
401	rpSerProAlaSerIleProGlyLysHisTy 4 :::	17 340
417	aValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL 4	34
434	euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 45	20

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vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:AAS97171
1591 AAGGGTGCATCGCCTGGAACAGCCCTGCCTGCAGGCGAGTGGGAGACTGT 1640
                                                                                                                                                                                                                             1691 ACTTTGCCTCTTACCCCTGCAATCCCTGCCTTCTTCTCTGTTCCTGAG 1740
                                                                                                                                                                                                                                                                                                                                           2040
                                                                                    484
                                                                                                                                                                                                                                                                                                                                                                                                                                            LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa 517
                                                                                                                                                                                                                                                                              SnPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650
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                                                                                   uAlaValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAspT
                                                                                                                                                                                                                                                                                                                                                                                                                            584 luGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGlnGluProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cysteine protease partial DNA sequence #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAS97171 standard; cDNA; 1542 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2091 GGCAGTGATGAAA 2103
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alignment_block:
US-09-768-877-2 x AAS97171
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Quality: 2726.50
Ratio: 5.315
Percent Similarity: 85.358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAS97171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1542 BP; 259 A; 467 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 30; Figure 1F; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-041502/05.
P-PSDB; AAU72888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; limmune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder; ss.
                                            34
                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000; 2000US-201879P.
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                                                                                                                                                                                 1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17
aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                               CGCCTTCCCCGCCGCGACTCCTCGCCTCTTCTGCGACTTGTCTACGCCGC
                                                                                                                                                           ATGCGGGCGGGGCGCGACGCCGAGGGAGCTGTTCCGGGACGC
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                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                           Percent Identity: 85.358
                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 G; 266 T; 0 other;
                                                                                                                                                                                                                                           to: 1542
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CCACCIGCAGAGCCICIACACAGAGA	TGT-011E01CVSU1sThrArgAlai	w
yHisLeuGlnSerLeuTyrThrGluA 33 	lGlyTyrProValThrGluAlaGl	317 951
LeuArgGluPheAspGluLeuThrVa 317 	PheTrpValGluGluGluGluPhe	301 901
.euLeuSerGlnLeuGlnGluGlyGlu 300 	alaspalaalaValalaSerGluL 	284 851
rgGluGlyGlyGluGlyTrpSerGlnV 284 	gArgCysTrpGlnGlyLeuTrpAr 	267 801
iLeuArgIleGlnAsnProTrpGlyAr 267              	GlnAlaGlyGlnCysIleLeuLeu 	251 751
ValSerAspLeuArgGluLeuGlnGly 250 	euGlyGluPheHisAlaPheIleV 	234 701
euSerProArgAlaGlyAlaArgGluL 234 	7 nCysLeuileSerCysCysValLe 	217 651
SATGGInLeuLeuHisLeuLysAspGi 217 	GlyArgTrpGluHisArgThrCys	201
31ySerG1yG1yG1nG1nAspArgPro 200 	rgTrpAsnLeuLysGlyValAlag 	184 551
alaspLeuThrGlyGlyLeuAlaGlua 184 	aGlyGlnValAlaAspAlaLeuVa 	167 501
1HisGlySerTyrGluHisLeuTrpAl 167 	LeuGluLysValTyrAlaLysVal	151 451
ArgGluAspValPheTrpLeuProLeu 150 	rgLeuCysPheSerArgCysGlnA	134 401
spAspArgLeuProCysLeuAlaGlyA 134 	YArgTrpValGluValThrThrAs	117 351
rPheThrCysArgIleTrpGlnPheGl 117               CTTCACCTGTCGCATTTGGCAGTTTGG 35(	1 AlaAspGlnGluTyrArgGlySer 	101 301
VallleProProGlyGlnProSerTrp 100 	4 ysSerArgHisLeuLeuAspGlnv 	84 251
heLeuCysAlaCysAlaAlaLeuGlnL 84 	7 nGlyLeuLeuGlyAspCysTrpPh 	201
pAspProArgGluGlyGlnValLysGl 67 	1 AlaThrProArgLeuPheProAsp 	<b>51</b> 151

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1400
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                                                           384
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                                                                                                                                                                                                                                                                                                                                          467
                                                                                                                                                                                                                         rGlnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL 434
                                                                                                                                                                                                                                                                                  euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450
                                                                                                                                                                                                                                                                                                                                                                                                                                               484 rgValPheSerThrGlyArgValSerLeuSerAlaIleArgAlaValAla 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517 lGlnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerArgA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu 550
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                                                                                                             rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal
                                                                                                                                                                                                                                                                                                                                      451 TyrAspArgGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe
                                                                                                                                                                                                                                                                                                                                                       584 luGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGlnGluProLeu
                                                        eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 LysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 GlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1451 GAGTCTTCTCTACCGGCGAGTCTCCCTTAG......
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAD13883

seq\_documentation\_block:
ID AAD13883 standard; cDNA; 2180 BP.

AAD13883; SYSYEX

(first entry) 29-NOV-2001

Human calpain-like protease, 18036 cDNA.

Calpain-like protease 18036; spleen disorder; splenomegaly; lung; adult respiratory distress syndrome; colon; liver; jaundice; brain; idiopathic inflammatory bowel disease; cerebrovascular disease; acute meningitis; Albehimer's disease; T-cell; transplant rejection; systemic lupus erythematosus; skin; seborrhoeic keratosis; leukaemia; haematopoietic stem cell; heart; myocardial infarction; atherosclerosis; kidney; acute proliferative glomerulonephitis; urolithiasis; apoptosis; ischaemia; neurodegenerative disease; demyelinating disease; injury; EAE; experimental allergic encephalomyelitis; multiple sclerosis; spinal cord, human. chromosome dystrophy; proliferative disorder; cancer; gene therapy; chromosome 2; ss human;

Homo sapiens

Location/Qualifiers 183..1736 /\*tag=

NO: 3 in /product- "Calpain-like protease, 18036" /note- "This region is claimed as SEQ ID claim 1"

WO200164919-A2

07-SEP-2001.

26-FEB-2001; 2001WO-US06110.

28-FEB-2000; 2000US-0185333

(MILL-) MILLENNIUM PHARM INC.

(apeller-Libermann R;

WPI; 2001-565507/63. P-PSDB; AAE09756.

diagnosing, treating seven-transmembrane protein/receptor-related disorders and to identify modulators of therapeutic use New calpain-like protease polypeptides and polynucleotides for

Claim 1; Fig 1; 114pp; English

The invention relates to polypeptide and polynuclectide of calpain-like protease, 18036. The polypeptide and polynuclectide of the invention are useful for treatment and diagnosis of calpain-like protease-mediated disorders. These disorders include disorders of spleen (e.g. disopathic inflammatory bowel disease), liver (e.g. jaundice), colon (e.g. idiopathic inflammatory bowel disease), liver (e.g. jaundice), care include meningitis, Alzheimer's disease), T-cells (e.g. transplant disease, acute meningitis, Alzheimer's disease), P-cells (e.g. transplant rejection, systemic lupus erythematosus), skin (e.g. seborrhoeic rejection, atherosclerosis), kidney (e.g. acute proliferative (myocardial infarction, atherosclerosis), kidney (e.g. acute proliferative glomerulonephritis, urolithiasis), thymus, breast, testis, uterus, small intestine, disorders related to reduced platelet number, bone, covary, pain and infectious disorders. The molecules of the invention are also useful for diagnosing and treating disorders associated with perturbed cellular growth and differentiation, exercise-induced injury and repair, apoptosis, ischaemia, neurodegenerative diseases, demyelinating diseases including experimental allergic encephalomyelitis (EAE) and multiple solerosis, LGMD2A muscular dystroph, spinal cord injury, proliferative and differentiative diseases including experimental allergic encephalomyelitis chromosome of petworen minimizers in and protease, 18036 cDNA. The 18036 gene is located on chromosome of petworen man and petworen man and man an chromosome 2 between D2S140 and D2S2338 

Sequence 2180 BP; 395 A; 651 C; 764 G; 370 T; 0 other;

alignment\_scores:

alignment\_block:

567 OSerAspThrClubheHtsProTleClubheHtsTlePhoClubing co.		
551 GlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgPr 567		251 GlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyAr 267 
1460		234 euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 250 
lGlnLeu		
1460		1911 PASHIPULYSGIYVAIAIAGIYSETGIYGIYGINGINASPAIPPRO 
rqValPh		TOTERNATE LEAST PALALEUVALAS PLEUT INTOLYGLYGLYGLAGIUA
1460		
1460		
434 euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450		15
417 rGlnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnL 434		117 yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134
401 GlyaspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisTy 417 	· ·	101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117 
384 rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 400 		84 ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp 100 
eTrpLe		67 nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84
351 SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 367 		51 AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl 67 
334 rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 350 		34 euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys 50 
317 1G1yTyrProValThrG1uAlaG1yH1sLeugInSerLeuTyrThrg1uA 334 		17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
		1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17 
284 alaspalaalaValalaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 300 		19nment_block: S-09-768-877-2 x AAD13883 lign seg 1/1 to: AAD13883 from: 1 to: 2180
267 9ArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerglnV 284 		Quality: 2719.50 Length: 672 Ratio: 5.260 Gaps: 1 ercent Similarity: 76.935 Percent Identity: 76.935

567 oSerAspThrGluPheHisProIleGlyPheHisIlePheGlnValProG 584

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Method for screening for type 2 diabetes mellitus comprises detecting a polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otani K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of cDNA corresponding to a transcript of the human calpain 10 gene, CAPN10 (see AAZ27475).
                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA27478
                                                                                                                   1567
.....GICCCAG 1467
                                                                                                                                                      1568 CTGCCTGCGGGCACCTACAAGTTGTGCCTCCACCTACCTGCCGGACA 1617
                                                                                                                                                                                                          1618 CAGAGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATCC 1667
                                                                                                                                                                                                                                                                1668 ATTCACAGCAGGAGATGCTGGGCCAGTTCCTCCAAGAGGTCTCCGTCAT 1717
                                                                                                                                                                                                650
                                                                                          617
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                                                                                                                                                                                                                                                   667
                                                                                     584 luGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGlnGluProLeu
                                                 1468 AGGTGGAAGGAGCCAGGACGCACCCCACTGCTGCTGCAGGACCGCTG
                                                                                                                                                                                                                                              651 IleHisSerGlnGluMetLeuGlyGlnPheLeuGlnGluValSerValMe
                                                                                                                                         uLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAspT
                                                                                                                                                                                           634 hrGluGlyAlaPheThrValThrIleAlaThrArgIleAspArgProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIDDM1; non-insulin-dependent diabetes mellitus; CAPN1. calpain 10; calpain 10c; diapain-1; cysteine protease; chromosome 2; human; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oda N, Sreenan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 65; Page 224-225; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
42..1595
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAA27478 standard; cDNA; 2001 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horikawa Y,
                                                                                                                                                                                                                                                                                                                           1718 GGCAGTGATGAAACC 1733
                                                                                                                                                                                                                                                                                                   tAlaValMetLysThr 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human calpain 10c cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-339702/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bell GI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY79569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200023603-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAA27478;
                                                                                                               1518
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         1461
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The sequence contains an open reading frame that encodes a protein of 517 amino acids (see AAY79569), designated calpain 10c. The CAPN10 gene consists of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10b, respectively. Calpain 10c is encoded by exons 1-7 and 11-13 of the gene. It is readily detectable in many tissues, including skeletal muscle and islets. The invention of concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A G-to-A polymorphism in intron 3 of the CAPN10 gene in the NIDBM1 region of convenes are based on detection of a polymorphism in a calpain condition much are also claimed for: producing for a propensity for type 2 diabetes are based on detection of a polymorphism in a calpain condition are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polymorlectides, including the present sequence; identifying modulators of calpain activity using calpain 10 polypeptides and nucleic acids; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GGGCCTGCGGGATTGCTGGTTCCTGTGTCCCTGCGCCGCGCTGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2001 BP; 361 A; 602 C; 690 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 1
Percent Identity: 76.786
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Ratio: 5.252
nilarity: 76.935
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US-09-768-877-2 x AAA27478
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1191		142
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891		842
267 841	0-0	
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691		641
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6 <b>4</b> 1		592
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591		54:
541	2 CTGGAAAAGGTCTACGCCAAGGTCCATGGGTCCTACGAGCACCTGTGGGC	4

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-651 IleHisSerGlnGluMetLeuGlyGlnPheLeuGlnGluValSerValMe 667
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                                                                                                                            1477 CAGAGGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGCCATCC 1526
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                                                                                                                                             634 hrGluGlyAlaPheThrValThrIleAlaThrArgIleAspArgProSer
                                                                                                                                                                                                                                                                               601 LeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCysLe 617
                                                                                                                                                                                                                                                                                                                          567 oSerAspThrGluPheHisProIleGlyPheHisIlePheGlnValProG 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 snPheAlaSerTyrProThrAsnProCysPheProPheSerValProGlu 550
                                                                                                                                                                                                              617 uLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAspT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 GlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgPr 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 LysasnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa 517.
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                                                                                                                                                                                                                                                         CTGAGCTGCGTGCCACATCGCTACGCCCAGGAGGTGAGCCGGCTCTGCCT 1426
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH17182 seq\_documentation\_block:
ID AAH17182 standard; cDNA; 1534 BP.

AAH17182;

26-JUN-2001 (first entry)

Human cDNA sequence SEQ ID NO:16542

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens

EP1074617-A2

07-FEB-2001.

28-JUL-2000; 2000EP-0116126

nLeuLeuHisLeuLysAspGlnCysLeuIleSerCysCysValLeuSerP

210 202

Fri

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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oilgo-dT primer and an oilgouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oilgonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oilgonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oilgonucleotide comprising a sequence; complementary to a
polynucleotide which comprises a 1'-end sequence; where the
polynucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence, 3'-end sequence; where the
coligonucleotide which comprises at least 15 nucleotides and these defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
con particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
control of the full-length cDNAs. The primers are also useful for the
control of the full-length cDNAs. The primers allow obtaining of the full-length
control of AAH13631 to AAH13632
control of the primers allow obtaining of the full-length
control of the primers all of which are used in the exemplification
of the present thuman amino acid sequences; and AAH13632
                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the full-length cDNAs defined in the specification, and for the detand/or diagnosis of the abnormality of the proteins encoded by full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 16542; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                         Wakamatsu A, Nagai K,
                                                                                                                                                                                                                     Hayashi K,
                                                                                                                                                                                                         sogai T, Nishikawa T,
Sugiyama T, Wakamats
                                                                       2000JP-0118776,
2000JP-0183767.
                                                                                             02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
                                                   99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                  (HELI-) HELIX RES INST
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                                                                                                                                                                                                                Isogai T,
                                                                         11-JAN-2000;
                                                   27-AUG-1999,
                                                                                                                                                                                                              Ota T, Is
Ishii S,
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detection by the

<u>ب</u>

Yamamoto

Saito K, Ya

C; 507 G; 274 T; 0 other; Sequence 1534 BP; 286 A; 467

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160 ySerTyrGluHisLeuTrpAlaGlyGlnValAlaAspAlaLeuValAspL 177
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                                                                                                                                     144 AspValPheTrpLeuProLeuLeuGluLysValTyrAlaLysValHisGl
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               Length:
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            Quality: 2487.50
Ratio: 5.248
ilarity: 92.759
                                                                                                           to: AAH17182
                                                                                US-09-768-877-2 x AAH17182
                                      Percent Similarity:
alignment_scores
                                                                   alignment_block:
                                                                                                           Align seg 1/1
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260
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         SerGlnLeuGlnGluGlyGluPheTrpValGluGluGluGluPheLeuAr
                                                                                                                                                        gGluPheAspGluLeuThrValGlyTyrProValThrGluAlaGlyHisL
                                                                                                                                                                                       euGlnSerLeuTyrThrGluArgLeuLeuCysH1sThrArgAlaLeuPro
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                                                                                                                                                                                                                                                                                                                                 GGCCGGGCCCGGGCACTGGTGGTGACAGTCATACTTCGTGGAGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                               alGluLysArgArgValAsnLeuProArgValLeuSerMetProProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                      uLeuSerProGlyTyrTeuAlaValProSerThrPheLeuLysAspA
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227
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3 5.3	/number= 2 exon 52835479 /*tag= e	/number= 2 intron 3945.5282 /*tag= d	/number= 1 38133944 /*tag= c	/number= 1 /codon_start= 1375 intron	Key Location/Qualifiers exon 12351515 /*tag- a	Homo sapiens.	NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; GPR35 gene; G protein coupled receptor; human; polymorphism; UCSNP-43; chromosome 2; diapain-1; diagnosis; therapy; ds.	NIDDM1 region including CAPN10 and GPR35 genes.	15-AUG-2000 (first entry)	AAA27475;	_documentation_block: AAA27475 standard; DNA; 49136 BP.	seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA27475	644 ThrArgIleAspArgProSerIleHisSerGln 654 	627 roSerThrTyrLeuProAspThrGluGlyAlaPheThrValThrIleAla 643 	610 nGluValSerArgLeuCysLeuLeuProAlaGlyThrTyrLysValValP 627	594 LeuLeuGeuGlnGluProLeuLeuSerCysValProHisArgTyrAlaG1 610 	577 heHisilePheGlnValProGluGlyGlyArgSerGlnAspAlaProPro 593	560 rLeuHisGlaHisCysArgProSerAspThrGluPheHisProIleGlyP 577			laSerTyrProThrAsnProCys	
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The present sequence is that of a 49,136 bp region located within the NIDDM1 region of human chromosome 2. It includes the CAPNIO gene that encodes a novel calpain-11ke cysteine protease, designated calpain 10, and a gene encoding a G protein coupled receptor.

C GPR35. Alternative splicing of calpain 10 mRNA generates a family of proteins. Isoforms 10a-h (see AAY79567-74) are respectively concoded by exons 1-7,9-13, 1-7,11-13, 1-7,11-13, 1-7,11-13, 1-7,11-13, 1-7,11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-13, 1-7,9-13, 1-7,2-14,15 and 1,11-13. Calpain 10 mRNA is ubiquitously expressed; the major 2.7 kb transcript was detected in very human adult and foetal tissue examined. Mutations in the CAPNIO gene are responsible for susceptibility to type 2 diabetes. The nucleotide variant showing all the evidence for linkage to type 2 diabetes. There is alternative splicing of intron 3, but the molecular mechanism by which the polymorphism at UCSNP-43 affects susceptibility to type 2 diabetes in unclear. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based. Susceptibility to type 2 diabetes in unclear. Claimed methods for screening for a propensity for type 2 diabetes are based. Con detection of a polymorphism in a calpain encoding nucleic acid, for identifying modulators of calpain activity using calpain 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 2000-339702/29.
P-PSDB; AAY79567, AAY79568, AAY79569, AAX79570, AAY79571, AAY79572,
AAY79573, AAY79574, AAY79576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otani K;
                                                                                                                                                                                                                                                           "G-allele has a frequency of 0.71 in
non-Hispanic whites of German ancestry"
                                                                                                                                                                                                            "G-allele has a frequency of 0.75 in Mexican Americans"
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                                                                                                                                                                                                                                                                                                                                             /frequency= 0.94
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Asians (Japanese)"
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Sequence 49136 BP; 10300 A; 13118 C; 14165 G; 11553 T; 0 other;
polypeptides and nucleic acids, and using these modulators to diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.
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	498	aValalaLysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpG 	515
	7.17		
			531 11258
	532	SerArgAsnPheAlaSerTyrProThrAsnProCysPheProPheSerVa	548
	11259	AGCAGGAACTTTGCCTCATACCCCACCACCCTGCTTCCCCTTCTCGGT	11308
	548	ProGluGlyProGlyProArgCysValArgIleThrLeuHisGlnHisC 	565
	7	CONTRACTOR TO THE POST OF THE	2
	i in	7 SALY TOOCLASPING OLD THE STOOTEST PROHISTING TOOL TOOL TOOL TOOL TOOL TOOL TOOL TOO	580 11408
	580		80
	11409	AAGCTCCTTGCCCCAGGGAGGAGGGGGAGCAGAAGGGGCCCTCAGAG	
	580		580
	11459	TGCATCTTGGCCTCCATTGTCCCAACAGAGGGCTCTGGGCTCAGTC	11508
	580		280
	11509	CTGCCCTTCGAGGCGCTGCCTAGAACCCGCACAGGGC	11558
	580		580
	11559	CTCCCATCTCCAACCTCTAGAGGCAAGGCCGAAGATGGCCTCTGGA	11608
	580		280
	11609	AGGGCCGGGGCCTGGGAGGTGGGCAGGCTGATCCAGGCAGG	11658
	580		580
	11659	TCCAGAGGAGGTGGTGAGTGGGGAGGAAGGAAGTTTGGAGAGGACAG	11708
	580		280
	11709	GAGGCCGAGGTTGAGACCAGCGGGGGTGGGTCGAGCCCTGGCTTGGGAAC	11758
	580		280
	11759	GCAGGGGCTGATGGACTCAGGAGTGAGAGGAGGGGAGGCCCAGGCTGGC	11808

	647		647
	12708	CTATCTGTCCTGGCAGACCAGGGCTGTCCTGCCTACCTGGGGACCCTTCC	12659
	647		647
	12658	GTGCTCGCCTGTCCCCCCACGTCTCCTGCCTGCCCCTCACCCTCAAGCCC	12609
	647		647
	12608	GCTCTGGGACTTGGGGGCCGGCCAGCTGGAGGCTGGGGGTGCTGGAGTCTTA	12559
	647		647
	647 12558	PThrGluGlyAlaPheThrValThrIleAlaThrArgIleAsp                    CACAGAGGGGGCCTTCACAGTGACCATCGCAACCAGGATTGACAGGTGGG	633 12509
	633 12508	LeuLeuProAlaGlyThrTyrLysValValProSerThrTyrLeuProAs 	617 12459
	616 12458	euLeuSerCysValProHisArgTyrAlaGlnGluValSerArgLeuCys 	600 12409
	600 12408	OGluGlyGlyArgSerGlnAspAlaProProLeuLeuGlnGluProL 	583 12359
	583 12358	ACCCCAAGGCTGGCCCCCCTCAGTCTGAGCCTGCGCTTTCCTCAGGTCCC	581 12309
,	12308	CTCAAGAGGGCCAAGGGCATCCGAGCAGATGGCCCTGGGCTGGGCTCCCT	12259
	580		580
	12258	TCCAGTGTCCAGGCCTGGCAGCCCCTCCTCAGAGAAGGGGGCTGTATGTGA	12209
	580		580
*	12208	ACTGCCGGCACCTTCTGGCAAGGGTGGCCAGGCCTTGGTGAGGAGGCGAG	12159
	580		580
	12158	ACAGGTGTTAAAGCCCCCTGATGATGTGACAGGCCTCCAGGCGGGGGCCCCC	12109
	580		580
	12108	CCCTTGGGGC	12059
	580		580
	12058	CCCTCGCTGTTTGCCCTGGGCCACCGGCTCAGGTCCCCTAGAGCTCTGA	12009
	580		580
-	12008	GAAGGCACTGCAACCCTCGGTTCACAGTGGGCTGCCTGG	11959
	580		580
-	11958	GTTCATTCTCTGCAGACATGTGTCCCCTGGAATGCAGGGGCCCCT	11909
	580		580
-	11908	GCCAGCAGCCCCTGTCCACTTACCCTGACTCAGAATGACTGTGTCCCA	11859
	580		580
-	11858	** TGGCCACAGCAGCCCCTCGGGTGTGAGGAAGTCCACAGTCACTGAGCTCA	11809
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seq_documentation_block:
ID AAH04003 standard; cDNA; 874 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT;AAH04003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12709 TTGCTGGTCTGAGCCTGGAAGGAGTCTAGTGGGAGGTGGGCCCAGGAGC 12758
                                                                                                                                                                                                                                                                                                                                                                                                                                               12859 AAGAGGTG 12866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12759 ACACAGCÇACTTGTGTGACAAGTGCAGTCTGGGAGCGCTGATCTGGTGTC 12808
                                                                                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                     07-FEB-2001.
                                                                                                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                                                                               Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 InGluVal 664
                                                                                                                                                                                                                                                11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             Human cDNA clone (5'-primer) SEQ ID NO:838.
                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                            AAH04003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                               99JP-0300253.
                                                                                                                                                                                                                                                                      99JP-0248036
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs detection by the

Ota T, Ishii :

Isogai T, Sugiyama T,

Nishikawa T, Hayashi K, : T, Wakamatsu A, Nagai K,

Saito K, Otsuki H Yamamoto

s,

WPI; 2001-318749/34.

Claim 1; SEQ ID 838; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end complementary to a c particularly full-length cDNAs. The primers are also useful for synthesising polynucleotides, detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the proteins encoded by

705 GTACATTGGCCGTCCTTGCANAAGATCCAGGCTTGAACGCCGGCGGGACT

655 TINCCAGCAACCCCAAATTCTTGCTTGCGGGTCTCAGAACCGAATGAGGT

392 rp.....AlaGlyArgAlaArgAlaLeuValGly...AspSerHisThr 

```
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244
                                                                                                                                                                                                                                                                                                        145 ValPheTrpLeuProLeuLeuGluLysValTyrAlaLysValHisGlySe 161
                                                                                                                                                                                                                                                                                                                                                                     161 rTyrGluHisLeuTrpAlaGlyGlnValAla.AspAlaLeuValAspLeu 177
                                                                                                                                                                                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 yGlyGlnGlnAspArgProGlyArgTrpGluHisArgThrCysArgGlnL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 ACCGGCGCCTGGCAGAAGATGGAACCTGAAGGGCGTAGCAGGAAGCGG 154
                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GEGTTCTGGCTCCCCTTACTGGAAAAGGTCTACGCCAAGGTCCATGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                178 ThrGlyGlyLeuAlaGluArgTrpAsnLeuLysGlyValAlaGlySerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preuArgGluLeuGlnGlyGlnAlaGlyGlnCysIleLeuLeuArgI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 ArgAlaGlyAlaArgGluLeuGlyGluPheHisAlaPheIleValSerAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 874 BP; 161 A; 238 C; 315 G; 155 T; 5 other
                                                                                                                                                                                   Gaps: 7
Percent Identity: 86.364
                                                                                                                                                                                                                                                                             to: 874
                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                Ratio: 4.849
Percent Similarity: 90.210
                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAH04003
                                                                                                                                                               Quality: 1251.00
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US-09-768-877-2 x AAH04003
                                                                                                                                                  alignment_scores:
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      88888888
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH99362

BP.

CDNA; 751

seq\_documentation\_block:
ID AAH99362 standard;

AAH99362;

|::: 855 GGTT 858

421 yLeu 422

Human protein encoding cDNA sequence SEQ ID NO:197.

16-OCT-2001 (first entry)

406 SerTrpSerPro...AlaSerIleProGlyLysHisTyrGlnAlaValGl

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Whuman; cancer; ulcer; HIV infection; human immunodeficiency virus;
antibiflammancory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; cardiant; antianeamic; anaemic;
antigagregant; namostatic; vulnerary; antiulcer; osteopathic; eczema;
where antidepressant; noctropic; antiparkinsonian; infection;
meuroprotective; antidepressant; noctropic; antiparkinsonian; infection;
mentionaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
mentionaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
when the anaematopoletic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alserier's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM99166 to AAM99904 encode the human proteins given in AAM25255 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 386; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fang YT, Liu C, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM25421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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404 294 311

311 luPheAspGluLeuThrValGlyTyrProValThrGluAlaGlyHisLeu  328 GlnSerLeuTyrThrGluArgLeuLeuCysHisThrArgAlaLeuProGl 

504 327 554 344

361

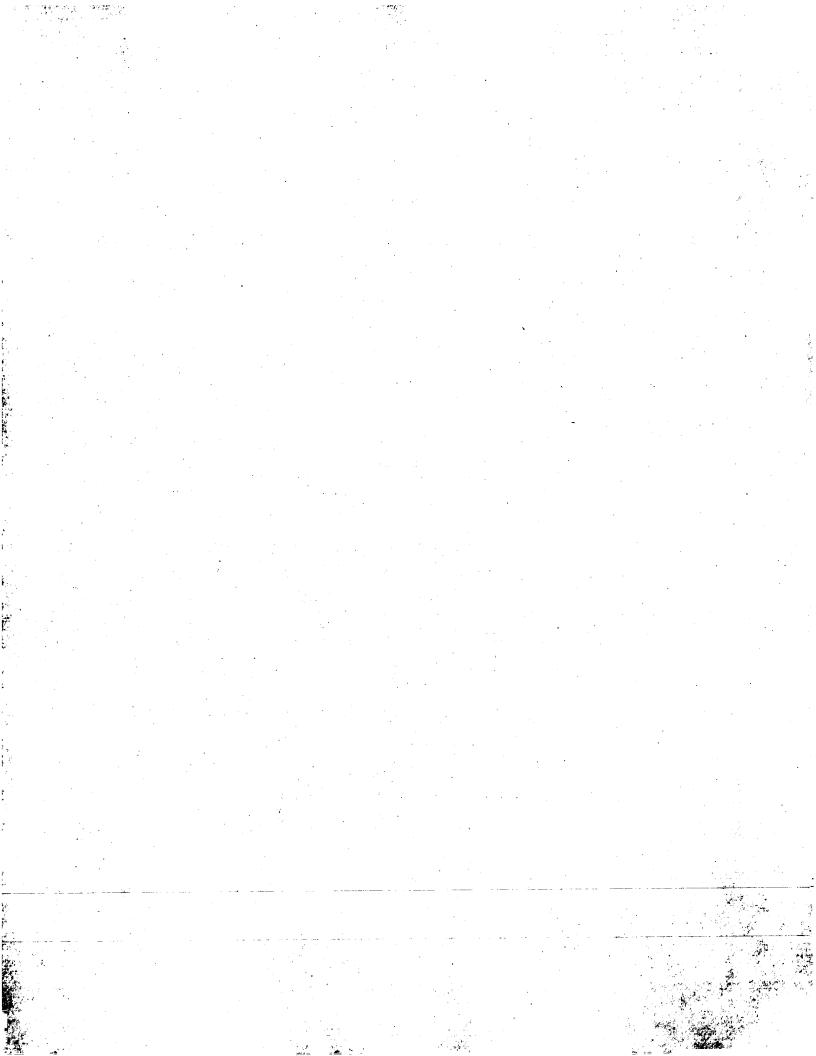
heProSerAsnProLysPhe.TrpLeuArgValSerGluProSerGluVa

361

alignment\_scores:
Quality:
Ratio:
Percent Similarity: CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides cc encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for cc agonists or antagonists of a protein and for the treatment and diagnosis. CC of disorders associated with the activity of a protein e.g. inflammation, cc rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, cc neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal canaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cc osteoprosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, cc neurological disorders. alignment\_block: US-09-768-877-2 x AAH99362 Align seg 1/1 to: AAH99362 452 402 210 193 352 176 302 160 252 143 202 126 pArgLeuProCysLeuAlaGlyArgLeuCysPheSerArgCysGlnArgG 102 TTCCTCCGGGACAGCCGAGCTGGGCCGACCAGGAGTACCGGGGCCTCCTTC Sequence 751 BP; 133 A; 219 C; 255 G; 144 T; 0 other; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiucer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic 93 GlySerTyrGluHisLeuTrpAlaGlyGlnValAlaAspAlaLeuValAs 176 pLeuThrGlyGlyLeuAlaGluArgTrpAsnLeuLysGlyValAlaGlyS 193 luAspValPheTrpLeuProLeuLeuGluLysValTyrAlaLysValHis 159 CCTGACCGGCGGCCTGGCAGAAAGATGGAACCTGAAGGGCGTAGCAGGAA 401 CCGCCTGCCGTGCCTTGCAGGGAGACTCTGTTTCTCCCGCTGCCAGAGGG leProProGlyGlnProSerTrpAlaAspGlnGluTyrArgGlySerPhe 109 AGGATGTGTTCTGGCTCCCCTTACTGGAAAAGGTCTACGCCAAGGTCCAT 301 964.00 5.446 90.769 from: 1 Gaps: 1 Percent Identity: 89.744 to: 751 Length: 195 251 143 151 51 76

rProArgAlaGlyAlaArgGluLeuGlyGluPheHisAlaPheIleValS 243

515	243	502
	243 erAspLeuArgGluLeuGlnGlyGlnAlaGlyGln 254	502 CCCCAGAGCAGGT51



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Page
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Cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-568-480-1+ 136.00 145
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Cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-646-715-31+ 132.00 170
Cgn2_6/ptodata/2/i
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Database sequences: 383533
Database length: 122816752
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Query length: 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score_list:
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22-869-3 + 3649.00 6014.72
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6.7e-172
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6.8e+0
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864
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; TYPE: DNA
; ORGANISM: Human
US-09-422-869-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 3649.00
Ratio: 5.430
Percent Similarity: 100.000
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                                                                                                                         428
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APPLICANT: POLICIANS, KENNETH S.
APPLICANT: ODA, NAOHISA
APPLICANT: HORIKAWA, YUKIO
APPLICANT: COX, NAOKISA
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: STEENAN, SEAMUS
APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS CRAIG L.
APPLICANT BELL GRAEME I
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEO ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-422-869-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09422869 Patent No. 6235481
                                                                                                                                                                                                                           TYPE 2 DIABETES
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US-09-768-877-2 x US-09-422-869-3 Gaps: 0
Percent Identity: 100.000

6

34 277

67 50 327

84 377

477 100 427

ualaglya 134            GCAGGGA 577	euProLeu 150            CCCCTTA 627	CeutrpAl 167	yLeualaglua 184 	spargPro 200            caggcca 777	LysaspGl 217 	aArgGluL 234             CCGGGAGC 877	uGlnGly 250            CCAGGGT 927	oTrpGlyAr 267 	SerGlnV 284              AGCCAGG 1027	uGlyglu 300           aggggag 1077	eurhrva 317           TCACCGT 1127	ThrGluA 334           ACAGAGA 1177	sGlyGln 350           GGCCAG 1227	roLysPh 367           CCAAATT 1277	LeuGlna 384 	aLeuval 400           ACTGGTG 1377	ysHisTy 417           AGCACTA 1427
nrThraspaspargLeuProCysLeual	ysGlnargGluaspvalPheTrpLeu	AlalysvalHisGlySerTyrGluHisLeuTrpA	pLeuThrGlyGl	1yvalAlaG1ySerG1yG1yG1yG1nG1nAs;	thrCysArgGlnLeuLeuHisLeu	sValLeuSerProArgAlaGlyAl	PhellevalSerAspLeuArgGluLeuGl	eLeuLeuLeuArgileGinAsnProf	uTrpArgGluGlyGlyGluGlyTrp(	SerGluLeuLeuSerGlnLeuGlnGluGly	1GluGluGluGluPheLeuArgGluPheAspGluLeuThrV.	ualaglyHisLeuglnserLeuTyrThrGl	rgAlaLeuProGlyAlaTrpValLysGly	GJyCysargasnasnserGlyPheProserasnPro	ProSerGluValTyrIleAlaVe	laAspTrpAlaGlyArgAlaArgAl	SerTrpSerProalaSerIleProGlyLysHisTr
/ yargirpyalgiuyalthrihraspasparg	rgLeuCysPheSerArgCysPhelserArgCysPhellillillillillillillillillillillillilli	LeuGluLysValTyr	aGlyGlnValAlaAspAlaLeuValAs	rgTrpAsnLeuLysG	GlyargTrpGluHisarg	nCysLeulleSerCysCy	euGlyGluPheHisAlaP	GlnAlaGlyGlnCysIle	gargCysTrpGlnGlyLeu	alaspalaalavalalas	PheTrpValGluGluGluGlu	lGlyTyrProValThrGlualaGlyHisLeuGlnS:	rgLeuLeuCysHisThrAr	SeralaGlyGlyCysargi	eTrpLeuArgValSerGlul	rgSerargLeuHisalaala	GlyAspSerHisThrSer7
117 528	134	151	167 678	184	201	217	234	251 928	267 978	284	301	317	334	351 1228	367	384	401

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1478 TGCCTAGGGTCCTGTCCATGCCCCCGTGCTGGCACCGCGTGCCATGCA 1527
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euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450
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                                                                                           TyrAspArgGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe
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                                                                                                                                                                                                                                                                                                                                              oSerAspThrGluPheHisProlleGlyPheHisIlePheGlnValProG
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Patent No. 623641
GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2178 GGCAGTGATGAAACC 2193
                                                                                                                                                                                                                                                                                                                                                                                                                                           667 tAlaValMetLysThr 672
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APPLICANT: ODA, NAOHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block
                              451
434
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; SEQ ID NO 13
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Human
US-09-422-869-13
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US-09-768-877-2 x US-09-422-869-13
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Quality: 3604.00
Ratio: 5.395
Percent Similarity: 99.257
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APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIGH I
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
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    151 LeuGluLysValTyrAlaLys.ValHisGlySerTyrGluHisLeuTrpA 167
                                                      442
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                                                                                                    YATGTTPVALGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134
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SREENAN, SEAMUS
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Percent Identity: 99.257
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167 laGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGlu 183

150 1379	LeuProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAl 4	<b>434</b> 1330
433	yrglnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsn 4	417
1329		1280
417 1279	IGlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisT 4 	1230
400 1229	ArgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVa	384 1180
383 <sup>°</sup>	7 heTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGln 3	367
1179		1130
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1129		1080
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1079		1030
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1029		980
317	uPheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrV	300
979		930
300	ValAspAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGl	284
929		880
283 879	7 rgArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGlyGluGlyTrpSerGln	83
267	yGlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyA	250
829		780
250	4 LeuGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGl	23
779		73
233	InCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGlu	217
729		680
217	0 oGlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspG	200
679		630
200	4 ArgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPr 	18 58
579	0 CCGGCCAGGTGGCCGATGCCCTGGTGGACCTGACCGGCGGCCTGGCAGAA	53

; TYPE: DNA ; ORGANISM: Human US-09-422-869-5

2297

LENGTH:

us-09-768-877-2.rni

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1579
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                             1480 CGAGTCTTCTCTACCGGGCGAGTCTCCCTTAGCGCCATCAGGGCAGTGGC 1529
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                                                              aLysAsnThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrV
                                                                              uGlyProGlyProArgCysValArgIleThrLeuHisGlnHisCysArgP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKANA, YUKIO
APPLICANT: CODA, NAOHISA
APPLICANT: CODA, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: CANO, YUN-ETNG
APPLICANT: CHOU, YUN-ETNG
APPLICANT: HANIS, CRAIG L.
APPLICANT: HELL, GRAEKE I.
ITILE OF INVENTION: METHODS OF TREATMENT OF
ITILE OF INVENTION: METHODS OF TREATMENT OF
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT APPLICATION NUMBER: 1999-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF
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EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2030 TGGCAGTGATGAAACC 2046
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rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
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                                                                                                                                                                                                                                                                                                                                                                            nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 GCCTTCCCGCGCGGGACTCCTCGCTCTTCTGCGACTTGTCTACGCCGC
                                                                                                                                                                                                                                                          eualaGlnPheargGluAspIleThrTrpArgArgProGlnGluIleCys
                                                                                                                                                                                                                                                                                                                                   192 GCCACACCCCGGCTGTTTCCAGATGACCCACGGGAAGGCCAGGTGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                       242 GGGGCTGCTGGGGGATTGCTGGTTCCTGTGTGCCTGCGCCGCGCGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 GACTCTGTTTCTCCCGCTGCCAGAGGAGGATGTGTTCTGGCTCCCCTTA
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                                                                                                                                                                     42 ATGCGGGCGGGCCGCGCGCGCGCGAGGGAGCTGTTCCGGGACCC
                                                                                                                                                                                                                                                                                     142 TGGCCCAGTTCCGCGAGGACATCACGTGGAGGCGCCCCCAGGAGATTTGT
                                                                                                                                                                                                                                                                                                                  AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                     ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl
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Gaps: 1
Percent Identity: 91.518
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                                                                                                                from: 1
                                                                                                              Align seg 1/1 to: US-09-422-869-5
                                                                  alignment_block:
US-09-768-877-2 x US-09-422-869-5
          3290.00
5.350
91.518
               Quality:
                                     Percent Similarity
alignment_scores
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US-09-768-877-2 x US-09-422-869-11	lignment	8 6 8 5 7 3 7 1 6 0 6 8 5 6 6	1522 1522

US-09-422-869-11

from: 1 to:

544	GlyGlySerArdAsnPheAlaSerTvrProThrAsnProCvs	528
1741	:	1741
527	laGlyGluTrpGlyThrValGlnLeuArgClySerTrpArgValGlyGl	511
1741		1741
511	rAlalleArgAlaValAlaLysAsnThrThrProGlyAlaAlaLeu	494
494 1740	LeuLeuArgValPheSerThrGlyA 	478
477 1691	1 euSerProGlyfyrTyrLeualaValProSerThrPheLeuLysAspala 	1642
ف ا		1592
461	GlyThrAlaCysHisAlaTyrAspArgGluValHisLeuArgCysGlu	44
444	8 GlulysArgArgValAsnLeuProArgValLeuSerMetProProValAl 	428
	TCTGGGACAGATACTGGCGCCAGGGCCAAGTGAAGCCCCGGGATT	1493
27	Va	427
426 1491	GCCTTTGTGGGCCCAGCTACAAGGAGGAC	1442
1441	GCAAAAGAAGTIGCIGGAAGGCCCACIGICCAGCAGCCCCCAGG	
426		42(
1391	<b>TTCCCTGTCCCTTCATGGATGTGGCCCACATGATGTTCCTTTCCTCT</b>	134;
426		42(
426	nalavalGlyLeuHisLeuTrpLys	41.
417	rpSerProAla 	124
400 1241	4 rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 	38,
384 1191	7 eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 	36.
367 1141	1 SeralaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh 	35.
350 1091	4 rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 	33,
334 1041	7 1GlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 	31.
317 991	1 PheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuThrVa 	30.

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alignment_block:
US-09-768-877-2 x US-09-422-869-9
                                                                                              alignment_scores:
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                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POLONSKY, KENNETH S
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEBAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
                                                                                                                                                                                                      SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Applic Patent No. 6235481
                                                                                                                                             TYPE: DNA
ORGANISM: Human
-09-422-869-9
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS OF TREATMENT OF FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                          APPLICANT: HANIS, CRAIG L. APPLICANT: BELL, GRAEME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGATTGACAGGCCATCCATTCACAGCCAGGAGATGCTGGGCCAGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eProPheSerValProGluGlyProGlyProArgCysValArgIleThrL
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                                                                                                                                                                                        2204
                                                                                Quality:
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Align seg 1/1
842
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                                                                                                                                                                                                                                                                                                                                                                             LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl
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                                                                                                                                                                                GTGTCTGATCAGCTGCTGCGTGCTCAGCCCCAGAGCAGGTGCCCGGGAGC
                                                                                                                                                                                                                                                                         GATGGAACCTGAAGGGCGTAGCAGGAAGCGGAGGCCAGCAGGACAGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGACCAGGAGTACCGGGGCTCCTTCACCTGTCGCATTTGGCAGTTTGG
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us-09-768-877-2.rni

317	lGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluA 334	
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334	rgLeuLeuCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGln 350 	
1092	SeradeuysiyyayayangashasaserdiyhherroserashproLysh) 367 	
367	rpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA 384	
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384	rgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuVal 400 	
401	lyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisT	
1242	GGTGACAGTCATACTTCGTGGAGCCCAGCGAGCATCCCGGGCAAGCACTA 1291	
417	rGlnalaValGlyLeuHisLeuTrpLysValGluLysArgArgValasnL 434 	
434	euProArgValLeuSerMetProProValAlaGlyThrAlaCysHisAla 450 	
45	AspargGluValHisLeuArgCysGluLeuSerProGlyTyrTyrLe 467	
1392	THE THE TRANSPORT OF TH	
467	ualaValProSerThrPheLeuLysAspalaProGlyGluPheLeuLeua 484 	•
484	rAlaileArgAlaValAla 5	
50	NSDThrThrProGlyAlaAlaLeuProAlaGlyGluTrpGlyThrVa 517	
1522		
517	lnLeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerAr	
1522	:	
534	PheAlaSerTyrProThrAsnProCysPheProPheSerValProG	
1522		
551	roGlyProArgCysValArgIleThrLeuHisGlnHisCysArgP	
1522		
267	isProlleGlyPheHisllePheGlnValF	
1523	GTCCA	
58 <b>4</b> 1530	luGlyGlyArgSerGlnAspAlaProProLeuLeuClnGluGluProLeu 600 	

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GENERAL INPORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NACHISA
APPLICANT: COX, NACHISA
APPLICANT: SREBNAN, SEAMUS
APPLICANT: SREBNAN, SEAMUS
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS, CANIS, JO.
APPLICANT: HANIS, CANIS, AND L.
APPLICANT: HANIS, AND L.
AP
                                                                                                                                                                                                                                                                                                  17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-422-869-19
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Percent Identity: 81.073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-768-877-2 x US-09-422-869-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 2963.00
Ratio: 4.756
nilarity: 92.846
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US-09-422-869-19
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51 AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl 67

	ATACGCGGACACTGCCTGGTGCCTGGGTGACAGGG
	7 IGLYTYPPROVALThrGLuAlaGlyHisLeuGlnSerLeuTyrThrG
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	284 alaspalaalavalalaSerGluLeuLeuSerGlnLeuGlnGluGlyGlu 300   :::
<b></b>	267 gArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnV 284 
	251 GlnAlaGlyGlnCysIleLeuLeuArgIleGlnAsnProTrpGlyAr 267    :::                     :::
•	234 euGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGly 250 
	217 nCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL 234 
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	134 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150 
	117 yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA 134
	101 AlaaspGlnGluTyrargGlySerPheThrCysArgIleTrpGlnPheGl 117 :::      :::
	84 ysSerArgHisLeuLeuAspGlnVall1eProProGlyGlnProSerTrp 100      :::
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134

117 yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA

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APPLICANT: OXA, NANCY J.

APPLICANT: COX, NANCY J.

APPLICANT: SEENAN, SEAMUS

APPLICANT: SREENAN, SEAMUS

APPLICANT: ZHOU, YUN-PING

APPLICANT: ZHOU, YUN-PING

APPLICANT: APPLICANT: ARBICH

APPLICANT: METHOR

TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

FILE REPERENCE: ARCD: 307

CURRENT FILING DATE: 1999-10-21

EARLIER APPLICATION NUMBER: 60/134,175

EARLIER PILING DATE: 1999-05-13

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTING DATE: 2001

EARLIER PILING DATE: 2001
                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-422-869-7
                                                                                                                                                                         Sequence 7, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH
APPLICANT: HORIKAWA, YUKIO
                         2091 GGCAGTGATGAAA 2103
                                                                                                                                                     seq_documentation_block
667 tAlaValMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Human
US-09-422-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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17 5 20 67 nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84 34 euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys 51 AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl Length: 672 Gaps: 1 Percent Identity: 76.786 to: 2001 from: 1 Align seg 1/1 to: US-09-422-869-7 US-09-768-877-2 x US-09-422-869-7 Quality: 2715.50 Ratio: 5.252 Percent Similarity: 76.935 alignment\_block

29

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1241
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                                                                     nCysLeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGluL
        aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA
                                                                                                                                    rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu
                                                                                                                           GlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                692 GIGICIGATCAGCIGCIGCTGCTCAGCCCCAGAGCAGGIGCCCGGGAGC
                                                                                                                                                                                                                                                        gArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl
                                                                                                                                                                                                                                                                                                                                                                                                                 351 SerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLysPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                   eTrpLeuArgValSerGluProSerGluValTyrIleAlaValLeuGlnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAspSerHisThrSerTrpSerProAlaSerIleProGlyLysHisTy
                             151
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alignment\_scores

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alignment_block:
US-09-768-877-2 x US-09-422-869-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-422-869-1 from: 1 to: 49136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: HELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF
FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 49136
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3910
                                                                                      4210 GGAGTCAGATCACCACGTTTAGAATAAAGAGACAAATGTGCCAGCTCACA 4259
                                                                                                                                                                                   4160 CATCAGGGAGGTTCGCCCTGCTCTGTGCTCTCTGACCCCCGGACTCCAT 4209
                                                                                                                                                                                                                                                                         4110 ACTCTGTCCCTCTGCTGCAGGGGGGGGGGTGCCTTGGCCTGCCAGAAGGCTC 4159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3960 CCTGTGTTTGTCCTGGAGCCGGTTTCTTTTTGCGTTTCTCCAGCCTGCTG 4009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3810 CAGGAGATTTGTGCCACACCCCGGCTGTTTCCAGATGACCCACGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4010 AGTACCAGGAGGCCTTGCGAAAGCAGAGCTGTGCCGCAGCCGGATCTCCT 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3860 GCAGGTGAAGCAGGGGCTGCTGGGGGATTGCTGGTTCCTGTGCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 yGlnValLysGlnGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysA 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCGCTGCAGAAGAGCAGGCACCTCCTGGACCAGGTGCGGGGCCCCTTC
GGAGGACGGGCTGGCTGGCAGCCTCTGCCTCAGATCTCTCCTCAGCTAG 4309
                                                                                                                                                                                                                                                                                                                                                                        GCTGTGTTGGGGGAAGGCAGAGAGTTCCAAGGCAGAGGCTGAGGACTGC 4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laAlaLeuGlnLysSerArgHisLeuLeuAsp.....
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Ratio: 3.224
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1310 CTCGCTGGTTTTCTTACAGGTTTTGAATATAAGTTTGCAAAAAGTTATTA 4359

90		06
4360	) AACCIGITICIGIGGGTAGACAGATACTCIGGGAGGAGAAGGCCTICTCA	4409
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90		06
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4510	TTCACTCATGTCCCAGGCCCCATGGTAAGCGTGTCACAGTCACTGGCTTT	4559
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5210	GGCCGGGACACTGGAGTAGCGCCGGGTGGTGCTTATATACACGCTCGCCTT	5259

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117 5360	yArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA : 	134 5409
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230 230	230 230
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7410 ATGAATATCACAGTAAACTGAAACAAGTTGTCATAGGCCTTGGTCTGGGT 7459	6510 GGAGGCCAGGACAGGCCAGGCCGCTGGGAGCACAGGACTTGTCGGCA 6559
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230 230	158ValHisGl 160
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230 230	157 157
7160 TTTTGAGTGCGCTCTCAGTTTTCCATGAGCACGCACGGTTTACGTGTTCC 7209	6260 ATGAGGAAGAAGGCAGAGGGAGTAAAGAGGTGGGATTGAGGCAGCGGTT 6309
230 230	157 157
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8360 ATTCCTCATGCAGGTGCCCGGGAGCTGGGGGGGGTTCCATGCTTCATTGT 8409	
242 ISerAspLeuArgGluLeuGlnGlyGlnAlaGlyGlnCysIleLeuLeuL 259 	
259 euarglleGlnAsnProTrpGlyArgArgCysTrpGlnGlyLeuTrpArg 275	
O TGCGGATCCAGAACCCCTGGGGCCGGCGGTGCTGGCAGGGGCTCT	
276 GluGly	
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277	
0 TTGGCTGTCTCCAGCAAGGCCCCTGAGTCCCTGCTCTCGTGACACATCC	
277	
8660 ITGICITGGCTCCAGGCAATCCTTGTGAGGCCTGGGACCAAGGTGGCCAT 8709	
277 277	
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277	
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277	
8810 GCTCCAGGGTGGCCGCTGCCCAGAAGGCCCTGTGCTGCAGAGCTGCTTCG 8859	
777	
8860 GCTGTGGGAGGGCTGCAGAGCTGGGGCACGGGGTCGCTGGCAGGAACTC 8909	

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,	8910	AGGGCTCTCTGGGTCCCCTCCAGGCTTCCCCCCCAGCCTGCCGGCAAGTTG	8959
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	8960	3GAGGGCTTCTGCTGAGATGAG	6006
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	9060	ACCTCCAGGAAGGGAGTTCTGGGTGGAGGAGGAGGAGTTCT	9109
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	S	CAGAGCCTCTACACAGGTAGTGCCCCG	9208
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	332		332
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	9409	TGAGGCCACCGTGGCGGGAGGCCAGCGAGG	9458
	333	TeuLeuCysHis	339
	9459	SCCTGGTGTTTTCTCAC	9208
	339	hrArgalaLeuProGlyAlaTrpValLysGlyGlnSerAlaGlyGlyCys 	355
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	, in	A SPANASHOEL OF THE COST AND TO THE TELEGRAP AS SECOND THE STATE OF THE SECOND TO THE SECOND THE SE	9608
	372	rGluProSerGluValTyrIleAlaValLeuGlnArgSerArgLeuHisA	389
	6096	AACCGAGTGAGGTGTACATTGCCGTCCTGCAGAGATCCAGGCTGCAC	9658
	389	laAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyAspSerHisThr 	405
	406	erTroserproA   a SerI   epros   vI well equant   avair   viv	, ,
	0	TCGTGGAGCCCAGCACCAGGCAACCACACACACACAGGCTGTGGGTCT	1 1
	422	isLeuTrpLysValGlu	428
	9759	CACCTCTGGAAGGTAACTCAGCCCCGTCTGGCTCACGCTCGGTTCAGCA	8086
	428		967

11609 AGGGCCGGGGGCCTGGGAGGTGGGCAGGGCTGATCCAGGCAGG		
580 580		428
11559 CCTCTCCCATCTCCAACCTCTCAGAGGCCAAGGCCGAAGATGGCCTCTGGA 11608	GCTGACAGGCCTTGGCGCTTTCATCTGTCAACTCCAGAGGCCCTTGTGCT 10708	10659 GCTGACAGGCC
580 580		428
11509 ACTTGGGCTCCCCCTGCCCTTCGAGGCGCTGCCTAGAACCCGCACAGGGC 11558	CCCGGGATTGGTGGGCATCTCTAGCTGGTCCCTGAGAGAGGGTGGAGGGT 10658	10609 CCCGGGATTGG
580 580	428	428
11459 AATTTGCATCTTGGCCTCCATTGTCCCAACAGAGGGCTCTGGGCTCAGTC 11508	ACTTGCAGGCTCGTGTCTGGGGACAGATACTGGCGCCCAGGGCCAAGTGAAG 10608	10559 ACTTGCAGGCT
580 580		428
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	12609 GTGCTCGCCTGTCCCCCACGTCTCCTGCCTCACCCTCAAGCCC 12658
	647 647
	12659 CTATCTGTCCTGGCAGACCAGGGCTGTCCTGCCTACCTGGGGACCCTTCC 12708
•	647 647
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	J. 5874 INFORM
•.	: SHINTANI, : NISHI, KAZ
	CANT: KAWAMOTO, TOR OF INVENTION: NOVE
	H (H)
	NDENCE ADDRES SEE: DIKE, B
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	:: E
,	ZIP: 02109 COMPUTER READABLE FORM:
	TYPE: D
	SYSTEM: DOS
	CATION DATA:
	4-
	CLASSIFICATION: 514 PRIOR APPLICATION DATA:
	APPLICATION NUMBER: 083649/1996
	ATION NUMBER:
	YAGENT INF
	NAME: Resnick, David S RECISTRATION NIMBER: 34 335
	I NUMBE
	TELEPHONE: 617-523-3400
	TELEFAX: 617-523-6440 TELEX:
	INFORMATION FOR SEQ. ID NO: 5: SEQUENCE CHARACTERISTICS:
•	LENGTH: 2109 base pairs

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-835-099A-5
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Ratio:
Percent Similarity:
236 luPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGlyGlnAla 252
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                                                                                                                                                                   655
                                                                                                                                                                             195 lyGlnGlnAspArgProGlyArgTrpGluHisArgThrCysArgGlnLeu 211
                                                                                                                                                                                                                                 624
                                                                                                                                                                                                                                           178 rGlyGlyLeuAlaGluArgTrpAsnLeuLysGlyValAlaGlySerGlyG 195
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                                                                                                                                                                                                                                                                                                           162 TyrGluHisLeuTrpAlaGlyGlnValAlaAspAlaLeuValAspLeuTh 178
                                                                                                                                                                                                                                                                                                                                                   128 uProCysLeuAlaGlyArgLeuCysPheSerArgCysGlnArgGluAspV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LeupheArgAspAlaAlaPheProAlaAlaAspSerSerLeu...PheCy 28
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                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCACCAAGAATGGACAGCTGCTCTTCCTACACTCGGAACAAGGCAATG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roGlyGlnProSerTrpAlaAspGlnGluTyrArgGlySerPheThrCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635.00
2.096
59.646
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Gaps: 17
Percent Identity: 32.283
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GlubheLeuLeuArgValPheSer 487 	roGlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAlaProGly 479             :::             	rAlaCysHisAlaTyrAspArgGluValHisLeuArgCysGluLeuSerp 463 	ValAsnLeuProArgValLeuSerWetProProValAlaGlyTh 446 :::::	alGlyLeuHisLeuTrpLysValGluLysArgArg 431 ::    :::::::       ::: TCGGCTATGCCGTCTACCAGGTTCCCAAGGAGCTGGAGAGTCACACGGAC 1341	rHisThrSerTrpSerProAlaSerIleProGlyLysHisTyrGlnAlaV 420 :       : CATGCTTAGC	LeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyAspSe 403         :::   ::::AGGTGGCGGAAGCGGATAGGACAAGG 1280	ValTyrIleAlaValLeuGlnArgSerArg 386      ::::::   ::::    TCGGTGAACCCTGCTGTACAGTGCTGCTGGGCCTGATGCAGAAAAATCGC 1254	OLYSPheTrpLeuArgValSerGluProSerGlu	GlyGlyCysArgAsnAsnSerGlyPheProSerAsnPr 365           :::	euCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGlnSerAla 352 ::	rProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluArgLeuL 336 :::::: ::::::::::::::::::::::::::::	ValGluGluGluGluPheLeuArgGluPheAspGluLeuThrValGlyTy 319 ::::: :::::   :::   :::   :::    ATGTCACTTTCAGATTTCGTGAGGCAGTTCTCTCGGTTGGAGATCTGCAA 1025	laAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGluPheTrp 302 :::       ::::::::::::	STrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnValAspA 286    :::        ::: ::   GTGGTCGGGAGCCTGGAGCGATGATGCACCAGAGTGGAATCACATAGACC 925	GlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyArgArgCy 269     :::   :::   ::::           :::     :::    ::::	::       :::    ::::   :::::   :::::    AGAGTCATGCGTACTCTGTCACTGGAGTCGAAGAGGTGAATTTCCAG 825

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 Fatent No. 6068990
 GENERAL INFORMATION:

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28 sAspLeuSerThrProLeuAlaGlnPheArgGluAspIleThrTrpArgA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GluGlyGlnValLySGlnGlyLeuLeuGlyAspCysTrpPheLeuCysAl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 rgProGlnGluIleCysAlaThrProArgLeuPheProAspAspProArg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 17
Percent Identity: 32.283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-157-349-5 from: 1 to: 2109
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APPLICATION NUMBER: US/09/157,349
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                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,099
                                                                                                                                                                                                                                                                                                                                                                                         97105508.2
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APPLICATION NUMBER: 97105508.2
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 4734,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-768-877-2 x US-09-157-349-5
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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2.096
59.646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-157-349-5
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Quality: (Ratio: Sercent Similarity: Sercent)
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FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
APPLICANT: SHINTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1281 CATGCTTAGC..... A 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205 TCGGTGAACCCTGCTGTACAGTGCTGCTGCTGGCCCTGATGCAGAAAAATCGC 1254
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KAWAMOTO, TOMOHITO
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 GluPheLeuLeuArgValPheSer 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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ELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                        REFERENCE/DOCKET NUMBER: 47342
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U:
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rAlaCysHisAlaTyrAspArgGluValHisLeuArgCysGluLeuSerP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alGlyLeuHisLeuTrpLysValGluLysArg......Arg 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyAspSe 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roGlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAlaProGly 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValAsnLeuProArg.....ValLeuSerMetProProValAlaGlyTh 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rHisThrSerTrpSerProAlaSerIleProGlyLysHisTyrGlnAlaV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGTTCTGCTTGAGAGTGTTCTCA 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Application US/08835099A 5874277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......AGGTGGCGGAAGCGGATAGGACAAGG 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISHI, Kaznori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHINTANI, Yasushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....ValTyrIleAlaValLeuGlnArgSerArg
                                                                                                                                                                                                      083649/1996
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1392

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1342

432

1292

420

403

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alignment_block:
US-09-768-877-2 x US-08-835-099A-6
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-835-099A-6 from: 1 to: 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                   601
                                                                                                                                                                162 TyrGluHisLeuTrpAlaGlyGlnValAlaAspAlaLeuValAspLeuTh 178
                                                                                                                                                                                                                                    145 alPheTrpLeuProLeuLeuGluLysValTyrAlaLysValHisGlySer 161
                                                                                                                                                                                                                                                                                                        501
                                                                                                                                                                                                                                                                                                                                     128 uProCysLeuAlaGlyArgLeuCysPheSerArgCysGlnArgGluAspV 145
                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GGATCTTGGA...CCAGGCTCTCCGCAAACTCAAGGCATCATCTGGAAGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 CTATTTAAGGACCCTGAGTTCCCAGCATGTCCATCAGCTTTGGGCTACAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LeuPheArgAspAlaAlaPheProAlaAlaAspSerSerLeu...PheCy 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 sAspLeuSerThrProLeuAlaGlnPheArgGluAspIleThrTrpArgA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2136 base par
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                           TATGAGGCTCTCGCTGGAGGTTCCACAGTGGAGGGGTTTGAGGATTTCAC
                                                                                                                                                                                                                                                                                                                                                                                   CAGTTCTGGCAGTACGGAGAGTGGGTGGTCATTGACGACAGGCT 500
                                                                                                                                                                                                                                                                                                                                                                                                              ArgIleTrpGlnPheGlyArgTrpValGluValThrThrAspAspArgLe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roGlyGlnProSerTrpAlaAspGlnGluTyrArgGlySerPheThrCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTGCCTCCCTGACCCTGAATGAAGAGCTGCTTTACCGGGTGGTCCCCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlyGlnValLysGlnGlyLeuLeuGlyAspCysTrpPheLeuCysAl 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyGlnGlnAspArgProGlyArgTrpGluHisArgThrCysArgGlnLeu 211
                                                                                   rGlyGlyLeuAlaGluArgTrpAsnLeuLysGlyValAlaGlySerGlyG 195
                                                                                                                                                                                                              AATTCTGGAGTGCCCTGCTGGAGAAAGCCTATGCCAAGCTTAATGGTTGT 600
                                                                                                                                                                                                                                                                                                GCCCACCAAGAATGGACAGCTGCTCCTTCCTACACTCGGAACAAGGCAATG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aCysAlaAlaLeuGlnLysSerArgHisLeuLeuAspGlnValIleProP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCACAGACATTTGTCAGGGTGGTCTAGGTGACTGCTGGCTTCTGGCTGC
                                           AGGTGGCATCTCTGAGTTTTATGACCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGACCAGGAC.....TTCCAGGAGAACTATGCGGGAATCTTTCACTTT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgProGlnGluIleCysAlaThrProArgLeuPheProAspAspProArg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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2.096
59.646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.283
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                                         681
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212 LeuHisLeuLysAspGlnCys.....LeuIleSerCysCysVal..

224

TGTGCGGGGTCTCTGCTGGGCTGCTCCATTGA

. AAACCACCAGCCAATCTATATCAGATCATCCGGAAGGCC

seq\_documentation\_block

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1003 ATGTCACTTTCAGATTTCGTGAGGCAGTTCTCTCGGTTGGAGATCTGCAA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 CCTGTCCCCGGACTCTCTGAGTAGCGAGGAGGTGCACAAATGGAACCTGG 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......ArgGluLeuGlyG 236
                                                                     236 luPheHisAlaPheIleValSerAspLeuArgGluLeuGlnGlyGlnAla 252
                                                                                            269 strpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGlnValAspA 286
                                                                                                                                                                                                                                                                                          286 laAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGlyGluPheTrp 302
                                                                                                                                                                                                                                                                                                                                                                   303 ValGluGluGluGluPheLeuArgGluPheAspGluLeuThrValGlyTy 319
                                                                                                                                                                                                                                                                                                                                                                                                                                           319 rProvalThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluArgLeuL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 GlyGlyCysArgAsnAsnSerGlyPhePro.....SerAsnPr 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 ......ValTyrIleAlaValLeuGlnArgSerArg 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 LeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyAspSe 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 rHisThrSerTrpSerProAlaSerIleProGlyLysHisTyrGlnAlaV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 alGlyLeuHisLeuTrpLysValGluLysArg.....hrg 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 ralacysHisAlaTyrAspArgGluValHisLeuArgCysGluLeuSerP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 roGlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAlaProGly 479
                                  756 TGTCTCCAGTGCAGCCGAAGCCATCACCAGCCAGAAGCTGGTTA
                                                                                                                                             253 GlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGlyArgArgCy
                                                                                                                                                                                                                                             432 ValAsnLeuProArg.....ValLeuSerMetProProValAlaGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1232 TCGGTGAACCCTGTACAGTGCTGCTGGGCCTGATGCAGAAAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 oLysPheTrpLeuArgValSerGluProSerGlu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1308 CATGCTTAGC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1519 GAGTTCTGCTTGAGAGTGTTCTCA 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluPheLeuLeuArgValPheSer 487
225 .LeuSerProArgAlaGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1282 .....
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seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-09-157-349-6

45 . 19 Sequence 6, Application US/09157349

Fatent No. 6068990

GENERAL INFORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomohiro
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18

CORRESPONDEMES ADDRESS:
ADDRESSE: DIRE, BRONSTEIN, ROBERTS & CUSMAN, LLP 13 LeuPheArgAspAlaAlaPheProAlaAlaAspSerSerLeu...PheCy 28 28 sAspLeuSerThrProLeuAlaGlnPheArgGluAspIleThrTrpArgA 45 rgProGlnGluIleCysAlaThrProArgLeuPheProAspAspProArg  $\tt GluGlyGlnValLysGluGlyLeuLeuGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyLeuLeuGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyGluGlyGluGlyGluGlyGluGlyAspCysTrpPheLeuCysAlGluGlyG$ Percent Identity: 32.283 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, STREET: 130 Water Street
CITY: Boston OPERATING SYSTEM: DOS SOFWARE: FSASLSO for Windows Version 2.0 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/09/157,349 FILING DATE:
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTONEY/AGENT INFORMATION:
NAME: RESISTRATION NUMBER: 34,235 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/835,099 Align seg 1/1 to: US-09-157-349-6 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 alignment\_block: US-09-768-877-2 x US-09-157-349-6 COMPUTER: IBM Compatible REFERENCE/DOCKET NUMBER: SEQUENCE CHARACTERISTICS: LENGTH: 2136 base pairs TYPE: nucleic acid STRANDEDNESS: double INFORMATION FOR SEQ ID NO: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette TELEFAX: 617-523-6440 2.096 59.646 linear FILING DATE: CLASSIFICATION: Quality: Ratio: Percent Similarity: 02109 alignment\_scores: STATE: M COUNTRY:

336 euCysHisThrArgAlaLeuProGlyAlaTrpValLysGlyGlnSerAla 352 ::::   :::::   :::::    1103 TCCTGTTCAAC	ATGTCACTTCAGATTTCGTGAGGCAGTTCTCTCGGTTGGAGATCTGCAA  rProvalThrGluAlaGlyHisLeuGlnSerLeuTyrThrGluArgLeuL				212 LeuHisLeuLysAspGlnCysLeuIleSerCysCysVal 224		178 rGlyGlyLeuAlaGluArgTrpAsnLeuLysGlyValAlaGlySerGlyG 195       ::::::    :::::	162 TyrGluHisLeuTrpAlaGlyGlnValAlaAspAlaLeuValAspLeuTh 178	145 alPheTrpLeuProLeuLeuGluLysValTyrAlaLysValHisGlySer 161	128 uProCysLeuAlaGlyArgLeuCysPheSerArgCysGlnArgGluAspV 145	112 ArgIleTrpGlnPheGlyArgTrpValGluValThrThrAspAspArgLe 128 ::::::      :::	95 roGlyGlnProSerTrpAlaAspGlnGluTyrArgGlySerPheThrCys 111	78 aCysalaAlaLeuGlnLysSerArgHisLeuLeuAspGlnValIleProp 95	307 CGCACAGACATTTGTCAGGGTGGTCTAGGTGACTGCTGCTTCTGGCTGC 356
alignment_scores: Quality: 513.50 Ratio: 4.755 Percent Similarity: 82.443 Percent Identity: 77.099	SOPTWARE: PAtentin Ver. 2.0  SEQ ID NO 15  LENGTH: 1267  TYPE: DNA ORGANISM: Human US-09-422-869-15	APPLICANT: HANIS, CRAIG L.  APPLICANT: BELL, GRAEME I.  TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE. REFERENCE: ARCD:307  CURRENT APPLICATION NUMBER: US/09/422,869  CURRENT FILING DATE: 1999-10-21  EARLIER APPLICATION NUMBER: 60/134,175  EARLIER FILING DATE: 1999-05-13	GENERAL INFORMATION:  APPLICANT: POLONSKY, KENNETH S.  APPLICANT: HORIKAWA, YUKIO  APPLICANT: ODA, NAOHISA  APPLICANT: COX, NANCY J.  APPLICANT: SREENAN, SEAMIS  APPLICANT: STOU, YUN-PING  APPLICANT: OTANI, KENICHI	seq_name: /cynz_o/plouata/z/lna/bB_COMB.seq:US-09-422-869-15 seq_documentation_block: ; Sequence 15, Application US/09422869 ; Patent No. 6234481 ; Patent No. 6234481	ი — ი	463 roGlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAlaProGly 479             :::	446 rAlaCysHisAlaTyrAspArgGluValHisLeuArgCysGluLeuSerP 463	432 ValAsnLeuProArgValLeuSerMetProProValAlaGlyTh 446 ::::::	420 alGlyLeuHisLeuTrpLysValGluLysArgArg 431 ::    ::	403 rHisThrSerTrpSerProAlaSerIleProGlyLysHisTyrGlnAlay 420 :	387 LeuHisalaAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyAspSe 403         :::   ::::: 1282AGGTGGCGGAAGCCGATAGGACAAGG 1307	377ValTyrIleAlaValLeuGlnArgSerArg 386	365 oLysPheTrpLeuArgValSerGluProSerGlu	1141 GGGGGCTGCCAGAACTACCCAGCCACGTACTGGACCAATCC 1181

Fri

from: 1

to: US-09-422-869-17

Align seg 1/1

US-09-768-877-2 x US-09-422-869-17

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431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ysSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 .....CTTCCTGCAGACTGGACTTGCAAGTCCAGCCTGTA.. 467
                                                                                                                                                                               17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                                                                                                                                                                                                                                                                                                                                                                           67 nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-422-869-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 yArgTrpValGluValThrThrAspAspArgLeuProCysLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 92
Gaps: 0
Percent Identity: 100.000
                                                                 to: 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE
                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09422869
Patent No. 6235481
                                                             Align seg 1/1 to: US-09-422-869-15
alignment_block:
US-09-768-877-2 x US-09-422-869-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: SREBNAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 5.130
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block
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LENGTH: 864
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alignment\_block

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No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Methods for Modifying the Production of
: a Polypeptide
S: 80
                                                                             597 nGluProLeuLeuSerCysValProHisArgTyrAlaGlnGluValSerA 614
                                                                                                  614 rgLeuCysLeuLeuProAlaGlyThrTyrLysValValProSerThrTyr 630
                                                                                                                                                                                                                                                            631 LeuProAspThrGluGlyAlaPheThrValThrIleAlaThrArgIleAs 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-928-692-16
581 GlnValProGluGlyGlyArgSerGlnAspAlaProProLeuLeuLeuGl
                    647 pArgProSerIleHisSerGlnGluMetLeuGlyGlnPheLeuGlnGluV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Mod
TITLE OF INVENTION: APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                          430 TCTCCGTCATGGCAGTGATGAAACC 455
                                                                                                                                                                                                                                                                                                                                                                                                    664 alSerValMetAlaValMetLysThr 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4700 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
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	lnGlyGlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrp 265	N
	34 uGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuG 249	234 2596
	19 LeuIleSerCysCysValLeuSerProArgAlaGlyAlaArgGluLe 234 	219 2549
	rgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuL    :::      TCTGGAAGCGACTTTACAGATCCTTTCACCAAG	202 2505
	85 pAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgProGlyA 202	185 2470
	69 GlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluArgTr 185 :::	. 169 2423
	52 luLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAlaGly 168      :::       :::::   :::   ::: 73 AGAAGGCGTATTTGAAATTGCGCGGAGGCTATGATTTTCCCGGAAGCAAT 2422	152 2373
	44	144 2323
	28 LeuProCysLeuAlaGlyArgLeuCysPheSerArgCysGlnArgGlu 143	128 2294
	YSArgileT    :::: TTCGCTTTT	111 2244
٠		101 2194
		2144
	LeuGlnLysSerArgHisLeuLeuAspGlnValIleProProGlyGl 9	82 2094 97
	68 lyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAla 81 :::	2044
	53 oArgLeuPheProAspAspProArgGluGlyGlnValLysGlnG 68 ::::::	53 1994
	43 TrpArgArgProGlnGluIleCysAlaThr	194
	n seg 1/1 to: US-08-928-692-16 from: 1 to: 4700	Align
	ment_block: 9-768-877-2 x US-08-928-692-16	alignmen: US-09-7
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ValGlyGlnThrAlaGlyGlySerArgAsnPheAlaSerTyrProThr 540 ::: ::	rgValGlyGlnThrAlaGly ::: :::          ACACCTTCGACGGCAGGT	524 3308
DAlaGlyGluTrpGlyThrValGlnLeuArgGlySerTrpA 524         ::::::                 ATTCAAGGGTCTTGG. 3307	aAlaLeuProAlaGlyGluTr	507 3293
AlaIleArgAlaValAlaLysAsnThrThrProGlyAl 507	AlaIleArg ::: AAAGCCCAAGATAAATACAT	495 3260
roGlyGluPheLeuLeuArgValPheSerThrGlyArgValSerLeuSer 494 :::         :::           ::::: ATCAAAACTTTACTTTGTCTGCCCTTCTCTACCTGCCCTGTACGGATGGCA 3259	roGlyGluPheLeuLeuArg ::::        ATCAAAACTTTACTTTGTCT	478 3210
GlyTyrTyrLeuAlaValProSerThrPheLeuLysAspAlaP 478	OGlyTyrTyrLeuA         ::::   CAGAACAACATACACAGTCG	463 3160
GGCCCCTATGTGGATTCCCCTAATACGCTCATGAGGTTAGAGATGCCCCC 3159	GGCCCCTATGTGGATTCCCC	457 3110
OProValAlaGlyThrAlaCysHisAlaTyrAspArgGluValHis 456	roProValAlaGlyThrAla	441 3092
GluLysArgArgValAsnLeuProArgV 	uTrpLysValGluLysArg/ ::::::::::::::::::::::::::::::::::::	424 3058
GlyLysHisTyrGlnAla	GlyLysHisTyrGlnAla :::         CTTGACGAATACCAAGCGA/	414 3008
LeuValGlyAspSerHisThrSerTrpSerProAlaSerIlePro 413	rgAlaLeuValGlyAspSei    :::    CTTCTAGGCAAGCA	397 2963
		2962
ValLeuGlnArgSerArgLeuHisAlaAlaAspTrpAlaGlyArgAlaA 397	aValLeuGlnArgSerArgl	380
AsnProLysPheTrpLeuArgValSerGluProSerGluValTyrIleAl 380       :::    ::: :      ::::: AACCCGCAGTTCGCAGTGTCAACCGAGAACGGTGGGATTGTCTGGTTA 2962	AsnProLysPheTrpLeuA:       :::    :::  AACCCGCAGTTCGCAGTGTC	364 2915
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ThrValGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrTh 332	-	316 2816
lyGluPheTrpValGluGluGluGluFheLeuArgGluPheAspGluLeu 315 		299 2766
pAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluG 299 	rGlnValAspAlaA ;:: CCTCTCTGCATCGC	282 2716
GYSTIPGINGlyLeuTrpArgGluGlyGlyGluGlyTrpSe 282	GlyArgArgCysTrpGln	266 2681
GACAATTACTCGTGAAAAACCCTTGG 2680	AAGGTCGCCGA	2646

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	AlaPheThrValThrIleAlaThrArgIle 646	637
3607	3558 CGGCTCATATACAATCGTCTGTTCCACATTCGCGCGGATCAACTTGGC 3607	3226
636	620 laGlyThrTyrLysValValProSerThrTyrLeuProAspThrGluGly 636	62(
3557	3508 TGGTGACTATCGCCGTGGTGGCTCCCTTGTGGAAAGAAGAGCTCTGGAAC 3557	3208
620	603 sValProHisArgTyrAlaGlnGluValSerArgLeuCysLeuLeuProA 620	909
3507	3482 CGCAGTCGCGACATAATCGCTGATAG 3507	3482
603	587 ArgSerGlnAspAlaProProLeuLeuGlnGluProLeuLeuSerCy 603	583
3481	3446TTATTCTGGTCCAATGGAAATCGTGTCGCGAGTA3481	3446
586	570 hrGluPheHisProlleGlyPheHisIlePheGlnValProGluGlyGly 586	57(
3445	ACGGA	340(
570	ArgCysValArgIleThrLeuHisGln	555
3405	3356 AACCCCCAATTTAGGTTGGAGATAGAGAATGACACAGATGTTTCACTCCT 3405	335
204	or new total control of the control	5

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9b_est2:BI410486
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9b_est2:BF310796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_htc:AK002548
gb_htc:AK013497
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gb_est2:BF310408
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Database length: -1841457050
Search time (sec): 1794.740000
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1.0e-105
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  | AK002548 MUS MUSCULUS AGULT | MAK013497 MUS MUSCULUS AGULT | MAK013496 60296596011 NCI_CGAP_I | BE390603 601284961F1 NIH_MCC_44 | B1412050 60295959671 NCI_CGAP_I | BE619302 601473184F1 NIH_MCC_21 | BC333889 602460221F1 NIH_MCC_17 | BC293992 601173172F1 NIH_MCC_17 | BC293992 601173172F1 NIH_MCC_17 | BC293992 601173172F1 NIH_MCC_17 | BC293992 601173172F1 NIH_MCC_17 | BC293992 60117317393F1 NIH_MCC_17 | BC293992 601177393F1 NIH_MCC_17 | BC29393 601670565F1 NIH_MCC_17 | BC29314067 NIH_MCC_17 | BC26168 60314748F1 NIH_MCC_19 | BC48804 603317408F1 NIH_MCC_19 | BC48804 603317408F1 NIH_MCC_19 | BC48804 603321408F1 NIH_MCC_19 | BC792086 60269703F1 NCI_CGAP_19 | BL48804 6032174074F1 NCI_CGAP_19 | BL486046 6032028634F1 NIH_MCC_19 | BC79206 601895608F1 NIH_MCC_19 | BC35646 602028634F1 NIH_MCC_19 | BC35646 602028634F1 NIH_MCC_19 | BC350929 60128519F1 NIH_MCC_68 | BC300299 60128519F1 NIH_MCC_19 | 
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US-09-768-877-2 x AL526645
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SOURCE
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ORIGIN
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VERSION
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LOCUS AL526645
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Mammalia; Eutheria; Primates
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Li,W.B., Gruber,C., Jessee,J
Full-Length cDNA libraries a
Unpublished (2001)
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL526645.1 GI:12790138
/tissue_type="neuroblastoma cells"
//lab_host="DH108"
//note="Organ: brain; Vector: pCMVSPORT 6: 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6: 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6: 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
41 a 274 c 341 g 149 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="CSODC020YC19"
/clone_11b="LTI_NFL003_NBC3"
                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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4.0e-44
3.2e-44
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o sapiens cDNA clone CSODC020YC19 5
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2 BF012190 us39d02.yl Soare

1 AA386629 vb54e03.rl Ko mo

2 AL580623 AL580623 LTI NFL

1 BB610838 BB610838 RIKEN f
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Length: 262
Gaps: 1
Percent Identity: 99.237

173

to: 908

- 34
- 27 50

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134 524 151 574 184

234

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1...887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerGlnLeuGlnGluGlyGluPheTrpValGluGluGluGluPheLeuAr 310
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Plate: LLAM1612 row: n column: 20
High quality sequence stop: 809.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGCGGGAGCTCCAGGGTCAGGCGGCCAGTGCATCCTGCTGCGG
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Gaps: 8
Percent Identity: 92.308
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Ratio: 4.559
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US-09-768-877-2 x BI916704
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NIH-MGC http://mgc.nci.nih.gov/.
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Email: cgapbs remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
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260

151 277 201

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT REFERENCE

DEFINITION

244

51

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:BG475966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspAlaProGlyGluPheLeuLeuArgVal.PheSerThrGlyArg Val 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alTyrIleAlaValLeuGlnArgSerArgLeuHisAlaAlaAspTrpAla 393
                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                        High quality sequence stop: 760.
Location/Qualifiers
                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                               842 bp mRNA linear EST 21-MAR-2001
602521077F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639579 5',
                                                                                                                               http://image.llnl.gov
Plate: LLCM1403 row: i column:
                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                            BG47596
                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                              GI:13408245
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ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).*
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alignment\_block: US-09-768-877-2 x BG475966 alignment\_scores: Align seg 1/1 to: BG475966 Percent Similarity: 209 gGlnLeuLeuHisLeuLysAspGlnCysLeuIleSerCysCysValLeuS 193 SerGlyGlyGlnGlnAspArgProGlyArgTrpGluHisArgThrCysAr AGCGGAGGCCAGGACAGGCCAGGCCGCTGGGAGCACAGGACTTGTCG Quality: Ratio: 1241.50 4.721 93.262 from: 1 to: Percent Identity: Length: Gaps: 282 11 91.135 51 226

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292 uLeuSerGlnLeuGlnGluGlyGluPheTrpValGluGluGluGluPheL
snSerGlyPheProSer..AsnProLysPheTrpLeuArgValSerGluP
||||||||||
| ACAGCGGCTTACCCCAAGGAACCCCAAATTCTGGCTGCGGGTCTCAGAAC
                                                                                                                                       euProGlyAlaTrpValLysGlyGlnSer.AlaGlyGly.CysArgAsnA
                                                                                                                                                                                    CACCTGCAGGAGCCTCTACACAGAGAGGCTGCTCTGCCATACGCGGGGGG
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                                                                                                                                                                                                                                  euArgGluPheAspGluLeuThrValGlyTyrProValThrGluAlaGly
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|CAGGGAGTTGGACGAGCTCACCGTAGGCTACCCGGTCACGGAGGCCGGC
                                                                                                                                                                                                                                                                                                                            luGlyGlyGluGlyTrpSerGlnValAspAla.AlaValAlaSerGluLe
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334 GGGCTGCTGGGGGATTGCTGGTTCCTGTGTGCTGCCTGCGCCGCGCTGCAGA 383
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        134 ATGCGGCGGGCGGGGGGGGGGCGGGGAGCTGTTCCGGGACGC 183
                                                                                                                                                                                                                                                                                            nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 ACGCTGGGTGGAGGTGACCACAGATGACCCCTGCCGTGCCTTGCAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  854 CCTGCCCTTTTTGTCCCGGGACCCGCGGAACTTCCAGGGTTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 ArgArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 yGlnAlaGlyGlnCysIleLeuLeuLeuArgIleGlnAsnProTrpGly.
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Inb="NIH_MCC_85"

/tissue_type="lymptoma, cell line"

/lab_host="bridlo" (phage-resistant)"

/note="organ: lymph; Vector: pcNV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.867 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases I to 999)

E I (bases I to 999)

S NIH-MCC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lide Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Loadian/Qualitiers

Loadian/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               AGENCOURT_6484888 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5554201 BM477401
439
                                                                                                       439 rMetProProValAlaGlyThrAlaCysHisAlaTyrAspArgGlu.Val 455
                                                                                                                                                                                       1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl 17
                                                                             423 isLeuTrpLysValGlu.LysArgArgValAsnLeuProArgValLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 9
Percent Identity: 76.873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 999
                                                                                                                                                                                                                                         456 HisLeuArgCysGluLeuSerProGly 464
                                                                                                                                                                                                                                                                                     799 CACCTGCGTAGTGAGCTCTCACCGGGT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM477401.1 GI:18526443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1170.00
Ratio: 4.661
Percent Similarity: 81.759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: BM477401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-768-877-2 x BM477401
                                                                                                                                                                                                                                                                                                                             seq_name: gb_est2:BM477401
                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BM477401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
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DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

533

583 167 633 184 683 200 733 216

803

237 853 250 266

953 283 988

903

alignment\_scores

BASE COUNT ORIGIN

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alignment_block:
US-09-768-877-2 x BI668734
                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:BI668734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
385 rArgLeuHisAlaAlaAspTrpAlaGlyArgAlaArgAlaLeuValGlyA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAW11791 row: b column: 19
High quality sequence stop: 738.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 738)
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B1668734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIDDW//4 738 bp mRNA linear EST 12-SEP-2001 603293173F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312178 5',
                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                               : 1163.00
: 5.035
: 95.062
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Percent Identity: 93.004
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 155
                                418
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REFERENCE
AUTHORS
                                                                         JOURNAL COMMENT
                                                                                                                                                                                           KEYWORDS
SOURCE
FEATURES source
                                                                                                                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 CTTCTCTACCGGGCGAGTCTCCCTTAGCGCCATCAGGGCAGTGGCCAAGA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 ValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuArgVa 485
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                                                                                                                                                                                                                                                                                                                                                        yGlyArgSerGlnAspAlaProProLeuLeuGlnGluProLeuLeuS 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspThrGluPheHisProIleGlyPheHisIlePheGlnValProGluG1 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuArgGlySerTrpArgValGlyGlnThrAlaGlyGlySerArgAsnPh 535
                                                                                                                                                                                                                                                                                                                                                                                                                TGGAAGGAGCCAGGACGCACCCCCACTGCTGCTGCAGGAGCCGTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eAlaSerTyrProThrAsnProCysPheProPheSerValProGluGlyP 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACACCGAGTTCCACCCCATCGGCTTCCATATCTTCCAGGTCCCAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaValGlyLeuHisLeuTrpLysValGluLysArgArgValAsnLeuPr 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lPheSerThrGlyArgValSerLeuSerAlaIleArgAlaValAlaLysA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACCACCCCGGGGCAGCCCTGCCTGCGGGGAGTGGGGGACCGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCCCAGCACCTTCCTGAAGGACGCGCCAGGGAG.TTCCTGCTCCGAGT
                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 787)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
                        BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, V
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                      prime, mRNA sequence. AL529373
                                                                                                                                                                                                                                                                  AL529373 LTI_NFL001_NBC4
                                                                                                                                                                                                                       AL529373.1 GI:12792866
Location/Qualifiers
1. .787
                                                                                                                                                                                                                                                                  Homo
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                                                                                                                                                                                                                                                                op mRNA
sapiens cDNA
                          Web
                          ••
                       www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                linear EST 13-FEB-2001 clone CS0DD006YA15 5
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/organism="Homo sapiens" /db\_xref="taxon:9606"

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BE8899733 769 bp mRNA 11near EST 20-OCT-2000 601512765F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914009 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9666"
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/note="corgan: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb.
a 262 c 238 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 769)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Afrc
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9735 row: a column: 18
High quality sequence stop: 696.
Location/Qualifiers
rce
                        485
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      184 rgTrpAsnLeuLysGlyyalAlaGlySerGlyGlyGlnGlnAspArgPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468 aValProSerThrPheLeuLysAspAlaProGlyGluPheLeuLeuArgV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 221
Gaps: 0
Percent Identity: 99.095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1 to: 769
                                                                                                                                                                                                                                                                                                                                                                                    BE889733.1 GI:10347351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1115.00
Ratio: 5.068
Percent Similarity: 99.548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BE889733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-768-877-2 x BE889733
                                                                                                                                                                                                                                               seq_name: gb_est2:BE889733
                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BE889733
                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                217 nCysLeu 219
                                                                                                                                                                                                     780 GTGKCTG 786
                                                                                                                                                                                                                                                                                                                                                                                                                             human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 aAlaPheProAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 GACTCTGTTTCTCCCGCTGCCAGAGGGAGGATGTGTTCTGGCTCCCCTTA
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Gaps: 0
Percent Identity: 98.174
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Ratio: 5.380
Percent Similarity: 98.630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-768-877-2 x AL529373
                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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VERSION
KEYWORDS
                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:BF310408
                                                                                                                                                                                                               SOURCE
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                                                                                                                    TITLE
JOURNAL
                                                                                                                                              AUTHORS
                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 942)
                                                                                                                                                                                                                                                              mRNA sequence.
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US-09-768-877-2 x BF310408
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ORIGIN
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Plate: LLCM1011 row: i co
High quality sequence stop:
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cloned into ECORI/XhoI sites using the following 5/
edaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
93 a 250 c 347 g 152 t
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top: 718.
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Quality: 1106.00 Ratio: 4.337 Percent Similarity: 82.524 Percent Identity:

Length: Gaps:

4 77.346

Align seg 1/1 to: BF310408 from: 1 to: 942

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501

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sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610011119:calpain 10, full insert sequence. AK002548.1 GT:12832609
HTC; CAP trapper. Mus misculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (strain:C57BL/6J) adult male kidney cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library clone:0610011119.
                                                         HisTyrGlnAlaValGlyLeuHisLeuTrpLysValGluLysArgArgVa 432
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Alzawa, T., Baldarelli, R., Bono, H., Brownstein, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, Y., Nomura, K., Nomura, K., Nomuraki, R., Ohno, M., Okazaki, Y., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tajima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

K. Submitted (10-010-2012) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), Ringawa, 230-0045, Japan (F-mail:genome-reseges.riken.go.jp., Raxiel-1212, 1212, 1212, 1222, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1322, 1
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LISCSVLSPRAGTAMATTPSTISLLQRRKSVLERLSWLGVLLLPLL
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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data source:MGD, source key:MGI:1344392, evidence:ISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL
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                          rgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPro
                                                                                                                                                      aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 184
                                                                                                                                                                                                             LeuGluLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAl 167
                                                                                                                                                                                                                                                                                                       ysserArgHisLeuLeuAspGlnValILeProProGlyGlnProSerTrp 100
nCysLeuIleSerCysCysValLeuSerProArgAlaGly 230
                                                                                                                                       AGGGCAAGTGGCAGATGCTTTAGTGGATCTCACTGGAAGCCTGGCAGAAA
                                                                                                                                                                                                CTGGAAAAGGCCTATGCTAAGGTCCATGGATCGTATGAGCACCTGTGGGC
                                                                                                                                                                                                                                                    GACTCTGCTTTTCCCGGTGCCAGAGAGGATGTGTTCTGGCTTCCCTTA 548
                                                                                                                                                                                                                                                                    rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
                                                                                                                                                                                                                                                                                                                                                                TCTGACCAGAAATACCAAGGCTTCTTCACCTGTCGGATTTGGCAGTTTGG 448
                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGTCAACACCTCCTGGACCAGGTCTTCCCTCCAGGACAGCCAGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACACCTCAGCTGTTTCCAGATAACCCATGGGAGGGACAGGTGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCCCAGTTTCGGGAGGACATCACTTGGAGACGACCCCAGGAAATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCTGCTGGGAGATTGCTGGTTCCTGTGTCCTGTGCCGCCCTTCAGA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCATTCCCCGCCTCGGACTCCTCGCTCTTTTACAACTTGTCCACGCCTC
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Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                    Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute (10-JUL-2000) Yoshihide Hayashizaki, The Institute (10-JUL-2000) Yoshihide Hayashizaki, The Institute (10-JUL-2000) Yoshihide (10-JUL-2
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S (bases I to 1269)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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site (http://genome.gsc.riken.go.jp/) for

459 134 509 150 559 609

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629 200 217

184

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201 GlyArgTrpGluHisArgThrCysArgGlnLeuLeuHisLeuLysAspGl
                360 AGAGTCAACACCTCCTGGACCAGGTCTTCCCTCCAGGACAGCCAGGTTGG
                                                                       167 aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA
                                                                                                                                                                                                                                                                                               184 rgTrpAsnLeuLysGlyValAlaGlySerGlyGlyGlnGlnAspArgPro
84 ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp
                                                      101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 nCysLeulleSerCysCysValLeuSerProArgAlaGly 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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346 c 343 g 292 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
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                                                                                                                                                                                                                                                                                                                                                            .904
                                                                                                                                                                                                                                                                                                                                                                                                                       putative"
                                                                                                                                                                                          .1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AK013497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1091.00
Ratio: 5.005
Percent Similarity: 94.783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-768-877-2 x AK013497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                           FEATURES
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In unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remain.nh.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11289 row: i column: 15
High quality sequence store: 924.
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                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 1028)
NIH-MGC http://mgc.nci.nih.gov/.
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BI410486
BI410486.1 GI:15171409
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                                                                                                                                                                                                                                                                                                                                         house mouse.
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alignment_block:
US-09-768-877-2 x BI410486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1078.00
Ratio: 4.945
Percent Similarity: 94.372
                                                                                                                                                                                                                                  . 393
                            184
                                                                                              543
                                                                        167
                                                                                                                    151
                                                                                                                                          493
                                                                                                                                                               134
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                                                                                                                                                                                                                                                                            343
                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                          193 TGGCCCAGTTTCGGGAGGACATCACTTGGAGACGACCCCAGGAAATCTGT
                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GCCATTCCCCGCCTCGGACTCCTCGCTCTTTACAACTTGTCCACGCCTC
                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                    34 euAlaGlnPheArgGluAspIleThrTrpArgArgProGlnGluIleCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl 117
                                                                                                                                     GACTCTGCTTTTCCCGGTGCCAGAGAGAGGATGTGTTCTGGCTTCCCTTA
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                                                                                                                                                                                                                                                                                           YSSerArgHisLeuLeuAspGlnVallleProProGlyGlnProSerTrp 100
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                                                                                                                                                                                                                                                                                                                             nGlyLeuLeuGlyAspCysTrpPheLeuCysAlaCysAlaAlaLeuGlnL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 231
Gaps: 1
Percent Identity: 85.714
                                                                                                                                      542
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                                                                                                                                                                                                                             442
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                                                                                                                                                                                                                                                                                                                                                                                                          242
                                                                                                                                                                                                                                                                                                                                                                                                                               50
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Ratio: 5.462
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US-09-768-877-2 x BE390603
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52

Length: 197
Gaps: 0
Percent Identity: 100.000

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGTCTAATCAGCTGCTGTGCTTAGCCCCAGAGCAGGT 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE390603
BE390603.1 GI:9335968
EST.
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                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM256 row: j column: 15 High quality sequence stop: 600. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 601)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE390603 601 bp mRNA linear EST 21-JUL-2000 601284961F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606638 5',
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in the laboratory of Gerald M. Rubin (diversity of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
04 a 173 c 225 g 99 t
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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300

316

350

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134 rgLeuCysPheSerArgCysGlnArgGluAspValPheTrpLeuProLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 TCTGACCAGAAATACCAAGGCTTCTTCACCTGTCGGATTTGGCAGTTTGG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACTGGGAGGAAGTGACCATAGATGATCGTCTGCCTTGTCTTGCCGGGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGluLysValTyrAjaLysValHisGlySerTyrGluHisLeuTrpAl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aGlyGlnValAlaAspAlaLeuValAspLeuThrGlyGlyLeuAlaGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetArgAlaGlyArgGlyAlaThrProAlaArgGluLeuPheArgAspAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 aAlaPheProAlaAlaAspSerSerLeuPheCysAspLeuSerThrProL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaThrProArgLeuPheProAspAspProArgGluGlyGlnValLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AlaAspGlnGluTyrArgGlySerPheThrCysArgIleTrpGlnPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YArgTrpValGluValThrThrAspAspArgLeuProCysLeuAlaGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCTGCTTTTCCCGGTGCCAGAGAGGATGTGTTCTGGCTTCCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 70.934
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US-09-768-877-2 x BI412050
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                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

Enaldo, Ph.D.

ENAL Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

ENA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

ENA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be http://image.lnl.gov

Plate: LiAM11296 row: g column: 15

High quality sequence stort: 3

High quality sequence stort: 3

High quality sequence stort: 8

High quality sequence stort: 8

High quality sequence stort: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS B1412050
DEFINITION 602965960F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5121446 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 940)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                       YArgArgCysTrpGlnGlyLeuTrpArgGluGlyGlyGluGlyTrpSerG 283
                                                                                                                                                                                                                                                                     GluPheTrpValGluGluGluGluPheLeuArgGluPheAspGluLeuTh 316
                                                                                                                                                                                                                                                                                                                                                                                                    luLeuGlyGluPheHisAlaPheIleValSerAspLeuArgGluLeuGln 249
                                                                                                          202
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                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                     402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
                                                                                                                                                                                                                                     253 AGGTAGATGCAGCGGTAGCATCTGAGCTCCTGTCCCAGCTCCAGGAAGGG 302
                                                                                                                                                                                                                                                                                                                                      rValGlyTyrProValThrGluAlaGlyHisLeuGlnSerLeuTyrThrG 333
                                                                    283 InValAspAlaAlaValAlaSerGluLeuLeuSerGlnLeuGlnGluGly
                       103 AGCTGGGGGAGTTCCATGCCTTCATTGTCTCGGACCTGCGGGACCTCCAC
                                                                                                                                                                    203 CCGCCGCTCTGCAGGGCTCTGGAGGGGGGGGGGGTGAAGGGTGGAGCC
                                                                                                                                                                                                                                                                                                                                                      GlnSerAlaGlyGlyCysArgAsnAsnSerGlyPheProSerAsnProLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BI412050
BI412050.1 GI:15172973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BI412050
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157

34

17

20

207

29

257

307

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

84

117

134

507

557

source

FEATURES

AGGGCAAGTGGCAGATGCCTTAGTGGATCTCACTGGAAGCCTGGCAGAAA 607

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BASE COUNT
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KEYWORDS
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LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:BE619302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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                                                                                                                                                                                                                      source
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908 AGCGGACCTACGT 920
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                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9636 row: g column: 22
High quality sequence stop: 663.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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BE619302
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
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                 145
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Average insert size 1.8 kb. Library constructed by Li
Technologies. "
               Technologies.
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           295 g
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IMAGE:3876141 5',
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                                                        251 nAlaGlyGlnCysIleLeuLeuLeu.ArgIleGlnAsnProTrpGlyArg
                                                                                             607
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                                                                                                                                          557
                                                                                                                                               219 LeuileSerCysCysValLeuSerProArg.AlaGlyAlaArgGluLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 rProArgLeuPheProAspAspProArgGluGlyGlnValLysGlnGlyL
CTGATCAGCTGCTGCTCAGCCCCAGAAGCAGGTGCCCGGGAGCTGG
                                                                                                                                                                               AsnLeuLysGlyValAlaGlySerGlyGlyGlyGlnGlnAspArgProGlyAr
                                                                                                                                                                                                                                                                                    uLysValTyrAlaLysValHisGlySerTyrGluHisLeuTrpAlaGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGGCCAGTGCATC...CTGCTGTGGGATCAGAAACCCG...GGGGCG
                                                                                                                                                                                                                                                                                                                                                                 ArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrpAlaAs 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCCGGCTGTTTCCAGATGACCCACGGGAAGGGCAGGTGAAGCAGGGGC
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Ratio: 4.439
Similarity: 94.821
                                                                                                                                                                                                                              AACCTGAAGGGCGTAGCAGGAAGCGGAGGCCAGGACAGGCCAGGCCG
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Percent Identity: 92.430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="T cells from T cell leukemia"
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector Library was normalized. Library was constructed by
Life Technologies. Context: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                        EST 16-FEB-2001
                                                                                                                                                    Homo sapiens "Buthardata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 776)
14, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                    AL558905
AL558905 LIL_NFL008_TC2 Homo sapiens cDNA clone CS0DJ007YG13
                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ysSerArgHisLeuLeuAspGlnValIleProProGlyGlnProSerTrp 100
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                                                            prime, mRNA sequence.
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Ratio: 5.425
Percent Similarity: 98.469
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seq_documentation_block:
LOCUS AL558905
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TITLE
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Gapop 10.0 , Gapext 0.5
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1 MRAGRGATPARELFRDAAFP.
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US-09-422-869-28

US-09-422-869-14

US-09-422-869-16

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US-09-L57-349-1
US-08-835-099A-2
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US-09-422-869-22
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Compugen Ltd.
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(without alignments)
1120.409 Million cell updates/sec
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; TYPE: PRT
; ORGANISM: Human
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APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L:
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TY
FILE REFERENCE: ARCD:307
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CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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US-09-120-365-99
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US-09-120-365-96
US-09-120-365-94
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US-09-428-517-4
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US-08-804-227c-9
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US-09-515-039-95
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Pred. No. 0;
0; Mismatches
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PCT-US91-09784-2
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Result

and is Pred. No.

No.

Score

2963 2715.5 2701.5

2699 2336 858.5

672; 0,

Gaps

0

180

120 120 60 60

240 240 180

Minimum DB Maximum DB

Scoring table: Sequence:

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

97, Appl
95, Appl
96, Appl
98, Appl
99, Appl
99, Appl
96, Appl
96, Appl
197, Appl
197,

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Perfect score:

OM protein -

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GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTPLKDAPGE 480
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    541 NPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDAPPLLLQEPL
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Pred. No. 2e-264;
1; Mismatches 0;
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APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: ZHOU, YUN-PING
APPLICANT: ZHOU, YUN-PING
APPLICANT: HAMIS, CRAIG I.
APPLICANT: HAMIS, CRAIGHTON NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
BARLIER APPLICATION NUMBER: 60/134,175
ERRIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
CSOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09422869
Patent No. 6235481
GENERAL INFORMATION:
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76.88;
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Best Local Similarity 76.8
Matches 516; Conservative
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US-09-422-869-6
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                                               FWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG
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81.2%; Score 2963; DB 4;
Best Local Similarity 81.1%; Pred. No. 3.7e-289;
Matches 544; Conservative 45; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09422869
Fatent No. 6235481
GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: ODA, NACHISA
APPLICANT: COX, NANCY J.
APPLICANT: SKEENAN, SEAMUS
APPLICANT: SKEENAN, SEAMUS
APPLICANT: STEENAN, SEAMUS
APPLICANT: ALOU, YUN-PING
APPLICANT: HANIS, CRAIG I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: WEHODS OF TREATMENT OF J.
FILE REFERENCE: ARCD: 307
CURRENT FILING DATE: 1999-10-21
EGARLIER APPLICATION NUMBER: 60/134,175
SCOFTWARE: PATENT OF J.
SOFTWARE: PATENT OF J.
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US-09-422-869-18
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LENGTH: 666
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TYPE: PRT ORGANISM:

Human

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APPLICANT: HORIKAMA, YUKIO
APPLICANT: COX, NANCY J.
APPLICANT: GOX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: STEENAN, SEAMUS
APPLICANT: CTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
FILER OF INVENTION: MCTHODS OF TREATMENT OF TY
FILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER APPLICATION NUMBER: 50/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: PatentIn V SEQ ID NO 8 LENGTH: 513 TYPE: PRT

ORGANISM: Human

TITLE OF INVENTION: METHODS OF TREATMENT OF FILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
CARLIER FILING DATE: 1999-05-13
RUMBER: OF SEQ ID NOS: 30

TYPE

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DIABETES

APPLICANT: POLONSKY, KENNETH S
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J
APPLICANT: SREENAN, SEAMUS
APPLICANT: STANDAM YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L
APPLICANT: BELL, GRAEME I
APPLICANT: BELL, GRAEME I
APPLICANT: BELL, GRAEME I

GENERAL INFORMATION:

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Sequence 8, Application US/09422869 Patent No. 6235481

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                                              FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSDASIPGKHYQAV
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498; Conserv
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95.4%;
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5; Mismatches
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                                                                                                                                                                                         181 LAERWNLKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF 240
                                                                                                                                                                                                                                                                                          IVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGE 300
                                                                                                                                                                                                                                                                                                         FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV 420
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP 60
                                                                            23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP 60
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     Length 444;
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APPLICANT: ODA, NACHISA,
YUKIO
APPLICANT: ODA, NACHISA
APPLICANT: COX, NANCY J.
APPLICANT: ZHOU, YENANCY
APPLICANT: ZHOU, YUN-PING
APPLICANT: ZHOU, YUN-PING
APPLICANT: APPLICANT: CTANI, KENICHI
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
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  Score 2336; DB 4;
Pred. No. 2.3e-226;
1; Mismatches 0;
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Pred. No. 4.6e-78;
1; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
NUMBER OF SEQ. ID NOS: 30
SOFTWARE: PATENTIN OF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
  64.0%;
99.8%;
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81.7%;
                                Conservative
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Best Local Similarity 81.7
Matches 165; Conservative
                 Similarity
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421 GLHLWK 426
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  Query Match
Best Local Simi
Matches 425;
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TYPE: PRT
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                                                                                              Gaps
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GENERAL INFORMATION:
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: ODA, NAOHISA
APPLICANT: COA, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: GRAEN I.
APPLICANT: GRAEN I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: BALL, GRAEN I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARC. 307
CURRET FILING DATE: 1999-10-21
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10
LENGTH: 444
                                            Length 513;
                                                                      Indels
                                                                       8;
                                         Score 2699; DB 4;
Pred. No. 8.9e-263;
1; Mismatches 8;
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                                         74.0%;
98.2%;
                                      Ouery Match
Best Local Similarity 98.23
Matches 496; Conservative
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GENERAL INFORMATION:
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; ORGANISM: Human
US-09-422-869-10
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US-09-422-869-8
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US-08-835-099A-1
                                                                                                                                             Query Match
Best Local
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Patent No. 5874277
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for V
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
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MEDIUM TYPE: Diskett
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FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                            13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG 71
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                                                                                                                          Local Similarity es 164; Conserv
                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 0836 FILING DATE: 05'APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Resnick, David S
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     DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                                          LFKDPEFPACPSALGYKDLG-PGSPQTQGIIWKRPTELCPSPQFIVGGATRTDICQGGLG 103
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KAWAMOTO,
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                                                                                                                                      17.4%; Score 635; DB 2; 32.3%; Pred. No. 6.5e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND USE
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                                                                                                                      Mismatches 179;
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                                                                                                                                                   Length 703;
                                                                                                                   Indels 80;
                                                                                                                 Gaps
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US-09-157-349-1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: 1
                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                          APPLICATION NUMBER: 9710:
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 ATYWTNPQFKIRLDEVDEDQEESIGEPCCTVLLGLMQKNR-----
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                                                                                        REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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303 VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFP 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 GSGGQQDRPGRWEHRTCRQLLHLKDQC---LISCCV-LSPRAGA-----RELGEFHAFIV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ATYWTNPQFKIRLDEVDEDQEESIGEPCCTVLLGLMQKNR------RWRKRIGQGMLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AGRICESRCQREDVFWIPLIEKVYAKVHGSYEHIWAGQVADALVDITGGLAERWNIKGVA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 ------IGXAVYQVPKELESHTDAHLGRDFFLAYQPSARTSTYVNLREVSGRA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.4%; Score 635; DB 2; 32.3%; Pred. No. 6.6e-55;
                       APPLICALL...

PILIC DATE: 04-APR-1>>,
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: RESINICA, DAVIG S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 47342
TELECOMMUNICADICKET NUMBER: 47342
TELECOMMUNICADICKET NUMBER: 47342
TELECOMMUNICADICKET NUMBER: 47342
                 UMBER: US/08/835,099A
04-APR-1997
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Patent No. 6068990
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 32.39
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: sir
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US-09-157-349-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELSDEVRQFSRLEICNLSPDSLSSEEVHKWNLV1FN----GHWTRGSTAGGCQN---YP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGGQQDRPGRWEHRTCRQLLHLKDQC---LISCCV-LSPRAGA----RELGEFHAFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 WSPASIPGKHYQAVGLHLWKVEKR-----RVNLPR--VLSMPPVAGTACHAYDREVHLRC
                                                                                                                                                                             Length 703;
                                                                                                                                                                         Query Match 17.4%; Score 635; DB 3; Length 70
Best Local Similarity 32.3%; Pred. No. 6.5e-55;
Matches 164; Conservative 85; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08835099A
Patent No. 5874277
GENERAL INFORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
APPLICANT: NISHI, Kaznori
APPLICANT: NAWAMOTO, Tomohiro
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 ELSPGYYLAVPSTFLKDAPGEFLLRVFS 487
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-157-349-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY:
                                                                                                                                                                      Query Match
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LENGTH: 712 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 97105
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                       303 VEREEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGOSAGGCRNNSGFP 362
                                                                                    243 SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW 302
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APPLICATION NUMBER: US/09/157,349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
335 MSLSDFVRQFSRLEICNLSPDSLSSEEVHKWNLVLFN---
                                                       276 TGVEEVNFQ-GHPEKLIRLRNPWGEVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFW
                                                                                                                                                                               171 NGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTVEGFEDFTGGISEFYDLK---
                                                                                                                                                                                                            132 AGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KAWAMOTO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 130 W
CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                     54 LFKDPEFPACPSALGYKDIG-PGSPQTQGIIWKRPTELCPSPQFIVGGATRTDICQGGIG 112
                                                                                                                                                                                                                                                                                                                                     13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                          DCWLLAAIASLTLNEELLYRVVPRDQD--FQENYAGIFHFQFWQYGEWVEVVIDDRLPTK 170
                                                                                                                                               GSGGQQDRPGRWEHRTCRQLLHLKDQC---LISCCV-LSPRAGA-----RELGEFHAFIV 242
                                                                                                                                                                                                                                                                       DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                                                                                                                      -----KPPANLYQIIRKAL-----CAGSLLGCSIDVSSAAEAEAITSQKLVKSHAYSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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NISHI, Kaznori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                      17.4%;
32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 635; DB 3; Pred. No. 6.6e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 712;
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Best Local Similarity
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WVNPQFKIRLDETDDPDDYGDRESGCSFVLALMQKHR--

364 -- NPKFWLRVSEPSE--

339

EEFLREFDELTYGYPYTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFPS--KQV-NYRGQVVSLIRMRNPWGEVEWTGAWSDSSSEWNNVDPYERDQLRVKMEDGEFWNSF 338 RELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFWVEE SDLYQ------IILKALERGSLLGCSIDISSVLDMEAITFKKLVKGHAYSVTGA GSGGQQDRPGRWEHRTCRQLLHLKDQCLISC-----CVLSPRA-GARELGEFHAFIVSDL 245 DGKLVFVHSAEGNEFWSALLEKAYAKVNGSYEALSGGSTSEGFEDFTGGVTEWYELRKAP 231

RDFMREFTRLEICNLTPDA--LKSRTIRK--WNTTLYEGTWRRGSTAGGCRN---YPATF

391

434

305 279

-VYTAVLQRSRLHAADWAGRARALVGDSHTSWSP

280 246 232 192 172

72 DCWELCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131 55 LFRDEAFPPVPQSLGYKDLG-PNSSKTYGIKWKRPTELLSNPQFIVDGATRTDICQGALG 13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG

166;

Conservative

73;

Score 618.5; DB 4; Length 714; Pred. No. 3e-53; Indels 77

77;

Gaps

17;

16.9%;

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; ORGANISM: Human
US-09-422-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-422-869-22
                                                     SEQ ID NO 22
LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22,
                                                                                                                                                                                                                                           APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L
APPLICANT: BELL, GRAEME I
                                                                                           SOFTWARE: Patentin
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/422,869
                                                                                                                                                                                                         FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                        APPLICANT: ODA, NAOHISA APPLICANT: COX, NANCY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            atent No.
                                                                                                             NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                  APPLICANT: SREENAN, SEAMUS APPLICANT: ZHOU, YUN-PING
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: POLONSKY, KENNETH APPLICANT: HORIKAWA, YUKIO
                                                                                                                               EARLIER FILING DATE: 1999-05-13
                                                                                                                                               EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELSPGYYLAVPSTFLKDAPGEFLLRVFS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSPASIPGKHYQAVGLHLWKVEKR-----RVNLPR--VLSMPPVAGTACHAYDREVHLRC
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DCWFLCACAALQKSRHLLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCV-LSPRAGA----RELGEFHAFIVSDL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 PKFWLRVSEPSE------VYIAVLQRSRLHAADWAGRARALVGDSHTS--WSPA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG-FPSN 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 SIPGKHYQAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG 71
                                                ---EKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGEFLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAMA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTIOR: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.8%; Score 612; DB 4; 18est Local Similarity 31.2%; Pred. No. 1.3e-52; Matches 155; Conservative 87; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/422,869 CURRENT FILING DATE: 1999-10-21 EARLIER APPLICATION NUMBER: 60/134,175 EARLIER FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0 EENGTH: 703
                                                                                                                                                                                                                     573 VFSEKRNLSEEVENTISVDRPVKKKT 599
                                                                                                                                                               485 VFSTGR-----VSLSAIRAVAKNTT 504
                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: RAT
US-09-422-869-27
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                                          VLSPRAG-----ARELGEFHAFIVSDLRELQCQAGQCILLLRIQNPWG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CWFICACAALQKSRHILDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCLA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLA----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ERWNLKGVA------GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMYKIMKKAIERGSIMGCSIDDGTNMTYGTSPSGLNMGELIARMVRNM----DNSLLQDS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : : | | | | : | | | : | : | | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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31.4%; Pred. No. 4.38-53;
+ive 79; Mismatches 194; Indels 116;
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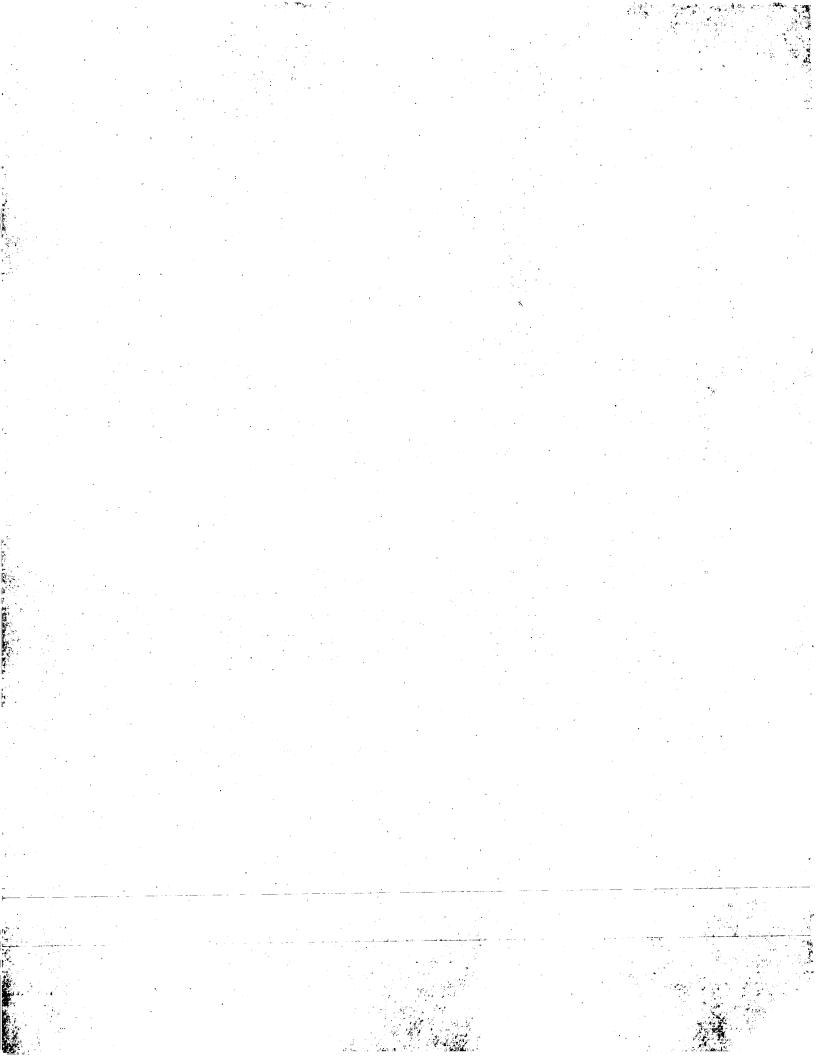
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE REFERENCE: ARCD: 307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER PAPPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO. 24
LENGTH: 821
         410 ASIPGKHYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAYD---
                                                                                                                           PGYYLAVPSTFLKDAPGEFLLRVF---STGRVSL 493
                                                                                                                                                         Sequence 24, Application US/09422869
Patent No. 6235481
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: POLONGKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: COXANI, KENICH
APPLICANT: ANNI, CRAIG L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 31.4%
Matches 178; Conservative
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; ORGANISM: Human
US-09-422-869-24
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		P. S
	09 LIJUWELKAKAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128	P 45
		B 4
15;	Similarity 30.4%; Pred. No. 8.4e-52; 7; Conservative 76; Mismatches 209; Indels 74; Ga	3 2 20 4
	Match 15 59. 6000 601. 17 1.	5
	; HYPOTHETICAL: NO US-08-726-525-7	US-
	TOPOLOGY: linear NOLECULE TYPE: protein	•• ••
	amino acid DNESS: sino	٠. ٠.
•	SEQUENCE CHARACTERISTICS: LENGTH: 700 amino acids	٠. ٠.
	INFORMATION FOR SEQ ID NO: 7:	•• ••
	TELEPHONE: (617) 498-8224	• ••
	CKET NUMBER:	٠. ٠.
•	REGISTRATION NUMBER: 32,724	٠
	Y/AGENT I	• • •
	APPLICATION NUMBER: 08/487,942 FILING DATE: 07-JUN-1995	
	CLASSIFICATION: 435 PRIOR APPLICATION DATA:	٠. ٠.
	7.	
	LICAT	
	<b>#</b>	٠. ٠.
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	٠. ٠.
	ER READABI	•••
	2	
	Clir: Cambridge STATE: MA	٠. ٠.
	7 5	• • •
	DENCE ADDRESS:	٠.
		٠. ٠.
LIGAND	OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF	٠. ٠
	CANT: Graham, James	٠.
	GENERAL INFORMATION: APPLICANT: Lin, Lih-Ling	
	SULT 15 -08-726-525-7	US RE
	489 STFEPFKDGDFC	₽
	Y 471 STFLKDAPGEFLLRVFS 487	QY
		5
	437 OTEKETERATURALI : : :	异

	477 LPGEVILVPSTFEPNKDGDFCIRVFSEKKADYQAV 512	477	Db
	461 LSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI 496	461	Qγ
476	429 IGFGIYEVPEELSGQTNIHLSKNFFLTNRARERSDTFINLREVLNRFK 476	429	Db
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405	VYIAVLQRSRLHAADWAG	357	Qy
375	326 MSFSDFLRHYSRLEICNLTPDTLTSDTYKKWKLTKMDGNWRRGSTAGGCR 375	326	В
356	R	303	Qy
325	267 TGAEEVESN-GSLQKLIRIRNPWGEVEWTGRWNDNCPSWNTIDPEERERLTRRHEDGEFW 325	267	DЬ
302	ASELLSQLQEGEFW	243	Оy
266	)KPPPNLFKIIQKALQKGSLLGCSIDITSAADSEAITFQKLVKGHAYSV 266	219	Db

Search completed: September 10, 2002, 10:40:13 Job time: 327 sec



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Q9GLG7 Q64698

Q9XSJ3 Q9N4B2

Q64698 rattus norv Q9n4b2 caenorhabdi Q9xsj3 oryctolagus O70376 rattus norv O70482 rattus norv Q9qzf9 rattus norv

008688 mus musculu Q91va3 mus musculu Q9g1g7 macaca fasc Q64698 rattus norv

Q91yu0 mus musculu Q9g1g2 macaca fasc Q9n185 bos taurus Q9n4b1 caenorhabdi sus scrofa gallus gall coturnix co

fasc

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070482

Q9GLG2

989800 Q91YU0

3 Q9YIC1 3 Q9YIC1 Q9N0M7 Q9N185 Q9N4B1

604.5 604.5 594.5 594.5 593.5 593.5 589.5

Q9TTH9 000263 1 008597 046596 1 09ER55 1 09ER55 1 09XSJ1 09Y8U6 09Y8U6

Q9xsjl bos taurus Q9tth8 ovis aries Q9v8u6 drosophila 046596 sus scrofa Q9er55 mus musculu

Q9xsj2 sus scrofa

ALIGNMENTS

16.9 16.8 16.8 16.8 16.8 16.7 16.7 16.7 16.7 16.3 16.3 16.3 16.3 16.3 16.3 16.3

Q9GLG1 008702 Q918G2

O9hbb1 homo sapien O9g1g1 macaca fasc O08702 rattus norv O918g2 brachydanio O9tth9 bos taurus

000263 homo sapien 088977 mus musculu

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Q9HC96 PRELIMINARY; PRT; 672 AA.
Q9HC96;
01-MAR-2001 (TIEMBLIEL 16, Created)
01-MAR-2001 (TIEMBLIEL 16, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
TYPE A CALPAIN-LIKE PROTEASE (CALPAIN 10).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

Homo sapiens (Human)

		RP S	SEQUENCE FROM N.A.
of results predicted by chance to have a	e to have a	RX P	PubMed~11017071;
qual to the score of the result being printed	t being printed,	RA H	N., Cox N.J., Li X.,
sis of the total score distribution.	ution.	RA H	Hinokio Y., Lindner T.H., Mashima H., Schwarz P., del Bosque Plata L.,
		RA H	Horikawa Y., Oda Y., Yoshiuchi I., Colilla S., Polonsky K.S., Wei S.,
SUMMARLES		RA C	Concannon P., Iwasaki N., Schulze J., Baier L.J., Bogardus C.,
		RA G	COOP L., Boerwinkle E., Hanis C.L., Bell G.I.;
		RT *	"Genetic variation in the gene encoding calpain-10 is associated with
15	Description	RT	type 2 diabetes mellitus.";
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RL N	Nat. Genet. 26:163-175(2000).
	Uyncyb homo sapien	RN [	<u> </u>
	Q96ji2 homo sapien	RP SI	SEQUENCE FROM N.A.
	0961g4 homo sapien	RC T	PISSUE-ENDOMETRIAL ADENOCARCINOMA;
	Q951p4 macaca tasc	RA St	Strausberg R.;
11 OPECE3	Q99313 mus musculu	RL SI	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
11 000000	Qyesks mus musculu	DR EI	EMBL; AF089088; AAG17966.1; ~.
o	Q9es66 rattus norv	DR EI	EMBL; BC004260; AAH04260.1;
	Quicy4 nomo sapien	DR H	HSSP; Q07009; 1DF0.
	Q9hc95 homo sapien	DR MI	MEROPS; C02.018;
	Q9hc93 homo sapien	DR I	nterPro; IPR001300; Peptidase_C2.
	Q9wvf0 mus musculu	DR I	InterPro; IPR000169; Thiolprot act site.
	Q9hc92 homo sapien	DR P	Pfam; PF01067; Calpain III; 2.
2	Q9cpy2 mus musculu	DR P	Pfam; PF00648; Peptidase C2; 1.
	Q9hc91 homo sapien	DR PI	PRINTS; PR00704; CALPAIN
13 001880	Q9er56 mus musculu	DR SI	SMART; SM00230; CysPc; 1.
. Katoto	VAIRED xenopus tae	DR PI	PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
. 73T010	Q918TU xenopus lae	DR PI	OSITE; PSO

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KIAA1845.
HOMO sapiens (Human).
BUKATYOTA MELAZOA; Chordata; Craniata; Vertebrata; El Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Last annotation update)
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                      9; DB 4;
8e-298;
                    100.0%; Score 3649;
100.0%; Pred. No. 8e-
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Best Local
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MEDLINE-21245130; PubMed-11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
*Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro. *;
DNA Res. 8:85-95(2001).
EMBL; ABOS9748; BAB47474.1; -.
1 1 1 SEQUENCE 705 AA; 78287 MW; 3B3BA9824FD0F53F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:2967328) (FRAGMENT).
                                                                                                                                               Score 3649; DB 4;
Pred. No. 8.6e-298;
Mismatches 0;
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Strausberg R.;
Strausberg RA;
Submitted (MAY-2001) to the EMB
EMBL; BC007553; AAH07553.1; -
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SEQUENCE 720 AA; 79586 MW;
   Q95LP4;
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Best Local :
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Hashimoto K., Osada N., Hida M., F
Terao K., Sugano S.;
"Isolation of novel full-length of
libraries.";
Submitted (OCT-2001) to the EMBL/C
EMBL; ABB072744; BAB69713.1; -.
Hypothetical protein.
SEQUENCE 653 AA; 72997 MW; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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NCBI_TaxID=9541;
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                                     NPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDAPPLLLQEPL
                                                                           MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
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Pred. No. 1.5e-275;
2; Mismatches 16;
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Bell G.I.;
"Genetic variation in the calpain 10 gene (CAPN10) is associated with type 2 diabetes.";
       REGOVKOGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 120
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                                                 MEDLINE-20472315; PubMed-11017071;
MEDLINE-20472315; PubMed-11017071;
MICKEWA Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hinokio Y., Linder T.H., Mashima H., Schwarz P.E.H.,
del Bosque-Platawa L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
Bajar L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_raxID=10090;
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Last sequence update)
Last annotation update)
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81.1%; Pred. No. 3.1e-240;
ive 45; Mismatches 76;
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InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
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Pfam; PF00648; Peptidase_C2; 1.
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EMBL, AF089089; AAG17967.1; -.
HSSP; Q07009; 1DF0.
                                                                                                                                                                                                                           Q9ESK3;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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655 LQEVSFMAVMK 665
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                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC005681; AAH05681.1; -.
EMBL; BC01069; AAH10969.1; -.
HSSP; Q07009; 1DF0.
                                                                                                                                              Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              THIOL_PROTEASE_CYS; UNKNOWN_1.
74596 MW; A0B1B37EE1DE2371 CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-LIVER, NORMAL. 5 MONTH OLD MALE MOUSE.;
                                                                                                                                                                                                                                                                                                      MGD: MGI:1344392; Capnio.
InterPro: IPR001300; Peptidase_C2.
InterPro: IPR001059; Thiolprot_act_site.
Pfam; PF01067; Calpain_III; 2.
Pfam; PF006488; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.2%
Matches 545; Conservative
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SMART; SM00230; CySPC; I.
PROSITE; PS00139; THIOL.
SEQUENCE 666 AA; 74596
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                                                                                                                               SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID-10090;
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Submitted (JUL-
                            CALPAIN 10
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MRAVRAETRARELFRDAAFPASDSSLFYNLSTPLAQFREDITWRRPQDICATPQLFPDNP

EVTTDDRLPCLAGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGG

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Best Local Similarity
Matches 544; Conserv
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MA H., Fuklage C., Kim Y.H., Duncan M.K., Reed Azuma M., Shearer T.R.;
"Characterization and Expression of Calpain 10 CALPAIN WITH NUCLEAR LOCALIZATION.";
J. Biol. Chem. 276:28525-28531(2001).
EMBL; AF227909; AAG09736.3; -.
HSSP; Q07009; 1DF0.
MEROPS; CO2.018; -.
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InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF01067; Calpain_III; 2.
Pfam; PF00668; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CYSPC; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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CALPAIN-LIKE PROTEASE 10.
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01-MAR-2001 (TrEMBLrel.
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MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
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81.1%;
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45; Mismatches 76;
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       LQEVSVMAVMK
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                                                                            GLHIWKVEKRKISLPRVLSAPPVAGTACHAYDREIHLRCELSPGYYLAVPSTFLKDVPGQ
                                                                                                              GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE
                                                                                                                                  FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV
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LQEVSFMAVMK
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RESULT Q9HC94
ID Q9
ID Q9
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ID Q9
ID Q1
ID Q
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SEQUENCE FROM N.A.

MEDLINE-20472315; PubMed-11017071;

Horikawa Y., Oda N., Cox N.J., Li X., Orh

Hinokio Y., Lindner T.H., Mashima H., Sch

A del Bosque-Plata L., Horikawa Y., Oda Y.

Polonsky K.S., Wei S., Concannon P., Iwa

A Polonsky K.S., Bogardus C., Groop L., Boerv
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Q9HC94;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CALPAIN-LIKE PROTEASE CAPNIOC.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
type 2 diabetes mellitus.",
Nat. Genet. 20:163-175(2000)..
EMBL; AF089091; AAG17969.1; HSSP: Q07009; 1DF0.
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                                                                                                                                                                                          "Genetic variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                          in the
                                                                                                                                                                                      gene
                                                                                                                                                                                      encoding calpain-10 is associated with
                                                                                                                                                                                                                                                                                   Boerwinkle
                                                                                                                                                                                                                                                                                                                          , Orho-Melander M., Hara M., Schwarz P.E., a Y., Yoshiuchi I., Colilla Iwasaki N., Schulze J.,
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Euteleostomi;

**.** s.,

DR DR DR KW

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1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
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                                                          SEQUENCE FROM N.A.
MEDLINE-20472315; PubMed-11017071;
MEDLINE-20472315; PubMed-11017071;
MEDLINE-20472315; PubMed-11017071;
HIORIO Y., Lindher T.H., Mashima H., Schwarz P.E.,
del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla
Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                               74.0%; Score 2701.5; DB 4; Length 544; ilarity 95.4%; Pred. No. 2.2e-218; Conservative 5; Mismatches 6; Indels 13;
       Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                        60656 MW; 17CE7B881A20855E CRC64;
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                                                                                                                                                                                                                                                                                                              PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1
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InterPro; IPR000169; Thiolprot_act_site.
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Pfam; PF00648; Peptidase_C2; 1.
       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                        544 AA;
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Best Local Similarity
Matches 498; Conserv
                                  NCBI_TaxID=9606;
                                                                                                                                                            Bell G.I.;
                                                                                                                                                                                                                                                                                                                                                           Protease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GIHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE 480
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                                                                                                                                                          517;
                                                                                                                                                          Length
                                                                                                              6761E4FAE4992910 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                          DB 4;
                                                                                                                                                     Score 2715.5; DB 4
Pred. No. 1.3e-219;
1; Mismatches 0;
                                                                                    UNKNOWN_1.
    MEROPS; CO2.018;
InterPro; IPR0001300; Peptidase_C2.
InterPro; IPR000168; Thiolprot_act_site.
Pfam; PP00648; Peptidase_C2; 1.
                                                                                 PROSITE; PS00139; THIOL_PROTEASE_CYS;
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Q9HC95;
Q9HC95;
Q1-MAR-2001 (TEMBLrel. 16, Crei
01-MAR-2001 (TEMBLrel. 16, Las;
01-DEC-2001 (TEMBLrel. 19, Las;
CALPAIN-LIKE PROTEASE CAPNIOB.
                                                                                                             517 AA; 57984 MW;
                                                                                                                                                    74.4%;
                                                                                                                                                    Query Match
Best Local Similarity 76.88
Matches 516; Conservative
                                                     PRINTS; PR00704; CALPAIN
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Best Local Similarity
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InterPro; IPR000169; Thiolprot_act_site.
Pfam; PP01067; Calpain_III; 1.
Pfam; PP00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
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Borikawa Y., Oda N., Cox N.J., Li X., Orhc
Hinokio Y., Lindner T.H., Mashima H., Sch
del Bosque-Plata L., Horikawa Y., Oda Y.,
Polonsky K.S., Wei S., Concannon P., Iwass
Baler L.J., Bogardus C., Groop L., Boerwin
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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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     481
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                                                                                                                                                                                                                                                                                                                                                                         241
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                                        IVSDLRELOGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGE
                                                                                                                                             FWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513 AA;
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092; AAG17970.1; -.
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98.2%;
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Pred. No. 3
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Iwasaki N., Schulze
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Schwarz P.E.,
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1.2e-218;
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Q9WVF0
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                                      421
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O9WVFO
O9WVFO;
O1-NOV-1999 (Tremblrel. 1
O1-NOV-1999 (Tremblrel. 1
O1-DEC-2001 (Tremblrel. 1
CALPAIN-LIKE PROTEASE.
   Protease.
SEQUENCE
                           InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PP01067; Calpain_III; 1.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CYSPC; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
                                                                                                                                                                    "Identification of a new cal
Submitted (FEB-1999) to the
EMBL; AF126867; AAD41779.1;
HSSP; Q07009; IDF0
MEROPS; C02.018; -
                                                                                                                                                                                                                                                TISSUE=LUNG;
Braun C., Seifert M.,
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    MGD; MGI:1344392;
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                          CAPN10 OR CAPN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLRVFSTGRVSLRSQRVEGARTHP
                                                                                                                                                                                                                                                                                     FROM N.A.
 605 AA;
                                                                                                                                                    Capn10.
                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
 67788 MW;
                                                                                                                                                                                                               Engel M., Welter C.;
new calpain-like cDNA in
to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                        12,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
85ACEE4A3FA0EB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                 mouse lung.";
databases.
CRC64;
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Query Match
Best Local s
Matches 490
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                                                                                                                                                                                                                                                                                                                                             1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
LAERWNLKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF
                                                                                                                                                                                                                                                                                 490;
                                                         FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV
                                                                                                                                         IISDLQELRSQTGQGILLLRIHNPWGRRCWQGLWREGGEGWNQVEPAKESELLAQLQEGE
                                                                                                                                                     IVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGBGWSQVDAAVASELLSQLQEGE
                                                                                                                                                                                                                                     EVTIDDRLPCLAGRLCFSRCQREDVFWLPLLEKAYAKVHGSYEHLWAGQVADALVDLTGS
                                                                                                                                                                                                                                                 EVTTDDRLPCLAGRLCFSRCQREDVFWLFLLEKVYÅKVHGSYEHLWAGQVADALVDLTGG
                                              FPCNPKFWLRLLEPSEVCVAVLQRPRRRL---VGQTRALAG---ASPAPVNLPGKDYQAV
                                                                                                                                                                                        LAERWSLKDVTKASGQQDRPSGGEHRTCRQLLHLKDRCLISCSVLSPRAGARELGEFHAF
                                                                                                                                                                                                                                                                                                                                  MRAVRAETPARELFRDAAFPASDSSLFYNLSTPLAQFREDITWRRPQEICATPQLFPDNP
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            73.7%;
80.7%;
                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                Score 2691; DB 11;
Pred. No. 1.9e-217;
3; Mismatches 68;
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                        480
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FWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG 360
                                              421 GLHLWK 426
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Q9CPY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bell G.I.;
"Genetic variation in the gene encoding calpain-10 is associated with
type 2 diabetes mellitus.";
Nat. Genet. 26:163-175(2000).
EMBL; AF089093; AAG17971.1;
HSSP; Q07009; 1DF0.
MEROPS; COLORS; COL
       540
                                                                       NPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDAPPLLLQEPL 600
                                                                                          LAERWNLKGVAGSGGQODRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF 240
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20472315; PubMed-11017071;
Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hinckto Y., Lindner T.H., Mashima H., Schwarz P.E., del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Spolonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J., Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
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64.0%; Score 2336; DB 4; Length 444;
Best Local Similarity 99.8%; Pred. No. 8e-188;
Matches 425; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CALPAIN-LIKE PROTEASE CAPNIOE.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M00230; CysPc; 1.
PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
                                                                                                                                                                                                                                                                       PRT;
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InterPro; IPR000169; Thiolprot_act
                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                          601 LSCVPHR 607
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595 LSCVPHR 601
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SEOUENCE
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ACCENCE TROWN N. A. STATE HIPPOCAMPUS, AND KIDNEY;

MEDLINE-21085660; PubMed=11217851;

A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Shburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli M., Barsh G.,

Bakai K., Okido T., Futuno M., Hume D.A., Kamiya M., Lee N.H.,

Brownstein M.J., Bult C., Retcher C., Fullita M., Monbaerts P.,

Ryons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez T., Sabanoto N.,

Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch R.-F,

Nyman-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wymshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
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264 Aa; 29946 MW; E8A530404A7E65F2 CRC64;
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1091; DB 11;
Pred. No. 1.4e-83;
1; Mismatches 21;
            264 AA
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InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00648; Peptidase_C2; 1.
                                                                    Created)
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86.1%;
                                                              (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK013497; BAB28883.1;
EMBL; AK002548; BAB22179.1;
HSSP; Q07009; 1DF0.
MEROPS; C02.018; -
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                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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SEQUENCE 264 AA;
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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09CPY2
09CPY2;
01-JUN-2001
01-JUN-2001
01-DEC-2001
CALPAIN 10.
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Best Local Simi
Matches 198;
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WEGQVKQGLLGDCWFLCACAALQKSQHLLDQVFPPGQPGWSDQKYQGFFTCRIWQFGHWE

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Best Local (
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type 2 diabetes mellitus.",
Nat. Genet. 26:163-175(2000).
EMBL; AF089094; AAG17972.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20472315; PubMed-11017071;
HOrikawa Y., Oda N., COX N.J., Li X., Orho-Melander M.,
Hinokio Y., Lindner T.H., Meshima H., Schwarz, P.E.,
del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I.,
Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze
Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis
Rell G. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-20472315;
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                                                                                                                                                                      LAERWNLKGVAGSGGQQDRPGR 202
                                                                                                                                                                                                                       EVITEDRLPCLAGRICFSRCQREDVFWLPLLEK---
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81.7%;
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Pred. No. 4.8e-64;
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Best Local S
Matches 170
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PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
SMART; SM00230; CysPc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS00018; B0588 MW; 37C07BDF0145B531 CRC64;
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01-DEC-2001
CALPAIN 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-20422668; PubMed-10964513;
Dear T.N., Meder N.T., Boehm T.;
"Gene structure, chromosomal localization Capni2, a new member of the calpain large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; CO2.017; -.
MGD; MGI:1891369; Capn12.
InterPro; IPR0021300; Peptidase_C2.
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EMBL; AJ289241; CAC10066.1;
HSSP; Q07009; 1DF0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2001
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                                                                                                    FWTNPQFRLTLLEPDEEEDDDDEEGPWGGWGAAGARGPARGGRVPKCTVLLSLIQRNRR-
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ADRSVFCARRDVSRRCRLPPGHYLVVPSASRVGDEADFTLRIFS
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1 (TrEMBLrel. 16,
1 (TrEMBLrel. 19,
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                                                  YLTVGFHVFQIPEELLDLWDSPRSRALLPGLL
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subunit gene family.";
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Search completed: September 19, 2002, 14:54:03 Job time: 282 sec

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(without alignments) 1918.845 Million cell updates/sec	September 19, 2002, 14:50:01; Search time 13.56 Seconds	OM protein - protein search, using sw model	Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: US-09-768-877-2 3649

Sequence: MRAGRGATPARELFRDAAFP.....SQEMLGQFLQEVSVMAVMKT 672

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

21 22 23 24 25 26 27 28 30 31	15 16 17 18 19	110 110 111 111 111	Result No. 1 2 3
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EMBL; AJ242832; CAB52137.1; -. HSSP; P17655; 1DKV.
MIM; 604822; -.

or send an email to license@isb-sib.ch).

InterPro; IPR002048; EF-hand.

InterPro; IPR001300; Peptidase\_C2.

InterPro; IPR001300; Peptidase\_C2.

InterPro; IPR001369; Thiolprot\_act\_site.

Pfam; PF001067; Calpain\_III; 1.

Pfam; PF00036; efhand; 2.

Pfam; PF000648; Peptidase\_C2; 1.

PRINTS; PR000704; CALPAIN.

SMART; SM00230; CYSPC; 1.

SMART; SM00230; CYSPC; 1.

SMART; SM00054; EFh; 2.

PROSITE; PS000139; THIOL\_PROTEASE\_CYS; 1.

PROSITE; PS00039; THIOL\_PROTEASE\_HIS; PALSE\_NEG.

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or send an email to license@isb-sib.ch).	and this statement is not removed. Usage by and for commercial	non-profit institutions as long as its content is in no	the European Bioinformatics Institute. There are no restrictions on its	between the Swiss Institute of Bioinformation	This SWISS-PROT entry is convright It is produced through a collineation		CALPAIN FAMILY OF THIOL PROTEASES.	Ď.	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCULA BINDING DOMAINS	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS	(regulatory) subunit.	catalytic) and a	ArgXaa with Leu or Val as the P2 residue	-!- CATALYTIC ACTIVITY: Preferential Cleavage Tyr-!-Yaa Met-!-Yaa	cytoskeletal remodelling and signal transluction		-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease	Genomics 5		NA levels in testis and located	Dear T.N., Moller A., Boehm T.:	MEDLINE=99339989; PubMed=10409436;	SEQUENCE FROM N.A.	[2]	NCBI_TaxID=9606;	Mammalia: Eutheria: Primates:	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata:		_	(CANP 11).	Calpain 11 (EC 3.4:22.17) (Calcium-activated neutral proteins	16-OCT-2001 (Rel. 40)	16-OCT-2001 (Rel. 40, Last		Q9UMQ6;	HIMAN STANDARD. DOT. 202	CANB HOMAN	SITT TO THE STATE OF THE STATE

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                                                                                                                                                                                                                                                                                                                                                                                                                  216 -----RPPQNLLRLLRKA--VERSSLMGCSIEVTSDSELESMTDKMLVRGHAYSVTG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415
                                                                                                                                                                                                                                                                                                                                                             191 AGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARE-----LGEFHAFIVSD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 LRELOGGAGOCILLIRIQNPWGRRCWOGLWREGGEGWSQVDAAVASELLSQLOEGEFWVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 HYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAY-----DREVHLRCELSPGYYLA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 EEEFLREFDELTVG--YPYTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG-F 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 WINPOFKISLPEGDDPED------DAEGNVVVCTCLVALMQKNWRHARQQGA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Gaps
                                                                                                                                                                                                                                                                                         12 ELFRDAAFPAADSSL-FCDLSTPLAGFREDITWRRPQEICATPRLFPDDPREGQVKQGLL 70
                                                                                                                                                                                                                                                                                                                 41 ELFEDPLFPAEPSSLGFKDLG-PNSKNVQNISWQRPKDIINNPLFIMDGISPTDICQGIL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 YODFLNNFTLLEICNLTPDTLSGDYKSYW-----HTTFYEGSWRRGSSAGGCRNHPGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 PSNPKFWLRVSE --- PSEVYIAVLQRSRLHAADWAGR --- ARALVGDSHTSWSPASIPGK
                                                                                                                                (POTENTIAL)
300640; THIOL_PROTEASE_ASN; FALSE_NEG.
Thiol protease; Calcium-binding; Multigene family.
17 207 THIOL PROTEASE DOMAIN I.
208 352 THIOL PROTEASE DOMAIN II.
                                                                                                                                                                                                                                        DB 1; Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Last sequence update)
LeCT-2001 (Rel. 40, Last annotation update)
Calpain, large [catalytic] subunit (BC 3.4.22.17) (Calcium-activate neutral proteinase) (CANP) (Mu/M-type).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                    17.7%; Score 644.5; DB 1; Length 7
33.7%; Pred. No. 1.6e-43;
.1ve 71; Mismatches 201; Indels
                                                           DOMAIN III, C2-LIKE DOMAIN.
                                                                                                                            ANCESTRAL CALCIUM SITE 3
ANCESTRAL CALCIUM SITE 4
                                                                                                                                                                                               3A618682B9674FAE CRC64;
                                                                                                                                                       SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                        705 AA
                                                                                                  EF-HAND 1.
EF-HAND 2.
                                                                                       DOMAIN IV.
                                                                        LINKER.
                                                                                                                                                        BY
BY
                                                                                                                                                                                               MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 VPSTFLKDAPGEFLLRVFS 487
                                                                                                                                                                                               80582
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                      353
515
515
586
616
681
102
259
702 AA;
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                 Best Local Sim
Matches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CANX_CHICK
P00789;
               Hydrolase;
                                                                                                                                                                               ACT_SITE
SEQUENCE
                                                                     DOMAIN
DOMAIN
CA_BIND
                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                     Query Match
                                                                                                             CA_BIND
                                                                                                                         DOMAIN
                                                          DOMAIN
                                                                                                                                         DOMAIN
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CANX_CHICK
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: THIS PROTEIN WAS PREVIOUSLY THOUGHT TO BE M-CALPAIN BUT HAS SINCE BEEN FOUND TO BE AN INTERMEDIATE FORM BETWEEN THE M AND
                                                                                                                                                                                                                                                                                                                                                                                  Emori Y., Ohno S., Tobita M., Suzuki K.;
"Gene structure of calcium-dependent protease retains the ancestral
organization of the calcium-binding protein gene.";
FEBS Lett. 194:249-252(1986).
                                                                                             к.;
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane upon Ca++ binding (By similarity).
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: Contains 5 EF-hand calcium-binding domains.
-!- SIMILARITY: BELONGS TO PEFPIDASE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87279982; PubMed=3038855;
Minami Y., Emori Y., Kawasaki H., Suzuki K.;
E.F. hand structure-domain of calcium-activated neutral protease (CANR) can bind Ca2+ ions.";
J. Biochem. 101:889-895(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of a third ubiquitous calpain species - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE-95260862; PubMed-7742367;
Sorimachi H., Isukahara T., Okada-Ban M., Sugita H., Ishiura S.
                                                                                                                                          fusion
                                                                           Ohno S., Emori Y., Imajoh S., Kawasaki H., Kisaragi M., Suzu
"Evolutionary origin of a calcium-dependent protease by fusi
genes for a thiol protease and a calcium-binding protein?";
Nature 312:566-570(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00230; CYSPC; 1.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00019; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_HIS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000169; Thiolprot_act_site
SEQUENCE FROM N.A.
MEDLINE-85061606; PubMed-6095110;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=86082358; PubMed=3000828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidase_C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 2.
Pfam; PF00648; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X01415; CAA25658.1; -.
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InterPro; IPR001300; Peptidas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00704; CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 А00979; СІСНН.
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MEROPS; C02.003; -.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit.
RP RX RA REPRESENTATION OF THE REPRESENTATIO
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Hydrolase;

protease; 213

Calcium-binding; Multigene THIOL PROTEASE DOMAIN I. THIOL PROTEASE DOMAIN II.

family.

DOMAIN III,

C2-LIKE

DOMAIN.

micromolar

Rapid

Submitted (MAY-2000)

Communication: nucleotide sequences of two isofocolar calcium-activated neutral protease 1 (mucalpoted (MAY-2000) to the EMBL/GenBank/DDBJ databases

two isoforms

o isoforms of porcine (mucalpain) cDNA.";

e

SEQUENCE FROM N.A. Simmen F.A., Vallet J.A.;

```
Query Match
Best Local S
Matches 162
                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9823;
                                                                                                       CANI_PIG STANDARD; PRT; 714 AA. P35750; Q29600; Q9N0M6; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Calpain 1, large [catalytic] subunit (EC 3.4.22.17) neutral proteinase) (CANP) (Mu-type) (muCANP) (Micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
CA_BIND
CA_BIND
DOMAIN
DOMAIN
                                                                             Sus scrofa (Pig).
                                                                                                                                                                                                                                         PIG
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                 SPGYYLAVPSTFLKDAPGEFLLRVFS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-SGFPSNPKFWLRVSEPSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEFWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERL-LCHTRALPGAWVKGQSAGGCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVSDLREL--QGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCWLLAAIGSLTLNEELLHRVVPHGQS---FQEDYAGIFHFQIWQFGEWVDVVVDDLLPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG
                                                                                                                                                                                                                                                                                                       PPGEYIVVPSTFEPHKEADFILRVFT 506
                                                                                                                                                                                                                                                                                                                                                                          GFAVYEVPEEAQGSQNVHLKKDFFLRNQSRARSETFINL---
                                                                                                                                                                                                                                                                                                                                                                                                         SWSPASIPGKHYQAVGLHLWK----VEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEFWMSFRDFMREFSRLEICNLTPDA-----LTKDELSRWHTQVFEGTWRRGSTAGGCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTAFKDVNYRGQQEQ----LIRIRNPWGQVEWTGAWSDGSSEWDNIDPSDREELQLKMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NPATFWINPQFKIKLLEEDDDPGDDEVACSFLVALMQKHR----
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705
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359
518
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534
5619
584
584
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                                       Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80351
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DOMAIN IV.

EF-HAND 1.

EF-HAND 2.

EF-HAND 3.

ANCESTRAL CALCIUM S

ANCESTRAL CALCIUM S

ANCESTRAL CALCIUM S

BY SIMILARITY.

BY SIMILARITY.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642; DB 1;
No. 2.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188;
                                                                                                           22.17) (Calcium-activated
(Micromolar-calpain).
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                                         Euteleostomi
Sus.
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                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                PRINTS; PR00704; CALPA:
SMART; SM00230; CysPc;
SMART; SM00054; EFh; 2
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01067; Calpain_III; 1. Pfam; PF00648; Peptidase_C2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                         CA_BIND
                                                                                                                                           DOMAIN
                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                 PROSITE; PS00018; PROSITE; PS00139;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF263610; AAF73444.1; -.
EMBL; F14611; CAA23154.1; -.
EMBL; U01180; AAA65125.1; -.
HSSP; P17655; 1DKV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- ENZYME REGULATION: Activated by micromolar concentrations calcium and inhibited by calpastatin.
-i- SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sun W., Ji S.Q., Ebert P.J., E
"Cloning the partial cDNAs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94146155; PubMed-8312396;
Sun W., Ji S.Q., Ebert P.J., Bidwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winteroe A.K., Fredholm Submitted (AUG-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Small intestine;
Winteroe A.K., Fredholm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochimie 75:931-936(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skeletal muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 528-623 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.
COFACTOR: Binds 3 calcium ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C02.
                                                                                                                                                                                                                                                 PS00640;
                                                                                                                                                                                                                                                                   PS00639;
                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .001; -
                                                                                                                                                                                                                             protease;
                                                                                                                                                                                                                                                                                                                                                      CALPAIN.
                                                                                                                                                                                                                                             THIOL_PROTEASE_CYS;
THIOL_PROTEASE_HIS;
THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                  EF_HAND;
   220
365
542
713
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609
639
674
704
115
272
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the EMBL/GenBank/DDBJ
                                                                                                                                                                      PROTEASE_HIS; FALSE_NEG.
PROTEASE_ASN; FALSE_NEG.
p; Calcium-binding; Multigene f
THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAIN
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EF-HAND 2.
EF-HAND 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AGRLCFSRCQREDVFWLPLLERVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
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                                                                                                                                                                                                                                                     Gaps
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008529; 035518; 054843;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millimolar-calpain) (80 kba M-calpain subunit) (CALP80).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 GSGGQQDRPGRWEHRTCRQLLH-----LKDQCLISC-----CVLSPRAGA-RELGEFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 --YPATEWVNPOFKIRLEETDDPEDDYGGRESGCSFVLALMOKHR-------RRERRF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 SGFPS----NPKFWLRVSE---PSEVY------IAVLQRSRLHAADWAGRARALVG
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MEDLINE-97480729; PubWed-9339374;
Dear N., Matena K., Vingron M., Boehm T.;
A new subfamily of vertebrate calpains lacking a calmodulin-like domain: implications for calpain regulation and evolution.";
Genomics 45:175-184(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 DSHTSWSPASIPGKHYQAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYD-----REV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                Length 714;
                                                                                                                                                                                                                                          75; Mismatches 182; Indels
                                                                                                               CRC64;
  V -> I (IN REF. 3).
I -> N (IN REF. 3).
E -> G (IN REF. 3).
S -> A (IN REF. 3).
S -> A (IN REF. 3).
                                                                                                                                                                                           Score 631; DB 1;
Pred. No. 1.9e-42;
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                                                                                                          81738 MW;
                                                                                                                                                                                  17.3%;
                                                                                                                                                                                                                                    Matches 167; Conservative
                                                                                                                                                                                                              Similarity
528
531
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714 AA;
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SEQUENCE FROM N.A.
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CONFLICT
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                                                                                                       SEQUENCE
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                                                                                                                                                                                                                    Local
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BR HSEAPE, COL 2002,

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BR HERPOS, COL 2002,

BR HGEPTO; IPRO02408; EF-hand.

BR HGEPTO; IPRO01609; Prinolprot_act_site.

BR HGEPTO; Calpain_III; 1.

BR HRWS; PRO07045, Calpain_III; 1.

BR HRWS; PRO07045, CALPAIN.

BR PRINS; PRO07045, CALPAIN.

BR SWART; SW00054; EFP; 2.

BR PROSITE; PRO0139; THIOL_PROTEASE_CYS; 1.

BR PROSITE; PRO0139; THIOL_PROTEASE_LS; FALSE_NEG.

BR PROSITE; PRO0640; THIOL_PROTEASE_CYS; 1.

BR PROSITE; PROOF THIOL_PROTEASE_CYS; 1.

BR PROOF THIOL_PROTEASE_CYS; 1.

BR PROOF THIOL_PROTEASE_CYS; 1.

BR PROOF THIOL_PROOF THIOL_PROTEASE_CYS; 1.

BR PROOF THIOL
                                                                                                                                                                         d Glass J.D., Nash N.R., Dry I., Culver D., Wesselingh S.;

"Cloning of m-calpain from mouse nervous system.";

"I substrated in the calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity).

"CATALYTE ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa or Arg-|-Xaa with Leu or Val as the P2 residue."

"COPACTOR: Binds 3 calcium ions."

"I ENZYMER REGULATION: Activated by 200-1000 micromolar concentrations of calcium and inhibited by calpastatin.

"I SUBGRIAT: Heterodimer of a large (catalytic) and a small concentrations of calculatory) subunit.

"SUBGRIAT: Activated by Calpainic, Translocates to the plasma membrane                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane upon Ca++ binding.
-! SIMILARITY: CONTAINS & EF-HAND CALCIUM-BINDING DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE 3 (POTENTIAL). SITE 4 (POTENTIAL).
                                                             Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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-> G (IN REF. 2).
-> G (IN REF. 1).
-> G (IN REF. 1).
682146B290968316 CRC64;
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Best Local Similarity 30.7
                                                                                                                                                                                                                                                                                                                                                                                   CANI_RAT STANDARD; PRT; 713 AA. P97571; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
                                                                                                                                                                                SEQUENCE FROM N.A.

MEDIJINE-97107433; PubMed-8950173;

Sorimachi H., Amano S., Ishiura S., Suzuki K.;

Primary sequences of rat mu-calpain large and respectively moderately and highly similar to Biochim. Biophys. Acta 1309:37-41(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAT
                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 SPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 DLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                      FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
CATALYTIC ACTYVITY: Preferential cleavage: Tyr-[-xaa, Met-[-xaa, Arg-]-xaa with Leu or Val as the P2 residue.
COPACTOR: BINDS 3 calcium ions (By similarity).
ENZYME REGULATION: Activated by micromolar concentrations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
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              calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W-----SPASIPGKHYQAVGLHLWKYEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPNTFWMNPQYLIKLEEEDEDEEDGERGCTFLVGLIQKHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NSGFPSNPKFWLRVSEPSE------VYIAVLQRSRLHAADWAGRARALVGDSHTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAEEVE-SSGSLQKLIRIRNPWGQVEWTGKWNDNCPSWNTVDPEVRANLTERQEDGEFWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAGSGGOODRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARE-----LGEFHAFIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLAGRICESRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGALFQDPSFPALPSSLGYKELGPYSSKTRGIEWKRPTEICADPQFIIGGATRTDICQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KPPPNLFKIIQKA--LEKGSLLGCSIDITSAADSEAVTYQKLVKGHAYSYT
                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.2%;
30.7%;
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Sciurognathi;
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Pred. No. 2.7e-42;
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            (catalytic)
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thi; Muridae;
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; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; AL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic; Translocates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALPAIN FAMILY OF THIOL PROTEASES.
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een the Swiss Institute of Bioinformatics and the EW
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PROSITE; PS00018; EF_HAND; 2.

PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                     Pfam; PF00036; efhand; 3.
Pfam; PF00048; Peptidase_C2;
PRINTS; PR00704; CALPAIN.
SMART; SM00030; CysPc; 1.
SMART; SM00054; EFh; 2.
                                                                                                                                                                             PROSITE; PS00640 Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   Pfam; PF01067; Calpain_III;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; U53858;
HSSP; P17655;
                                                                                                                                                                                                                                                                                                              InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site
                                                                                                                                                                                                                                                                                                                                                        MEROPS; C02.001
                                                                                                                                                                                                                                                                                                                                           [nterPro; IPR002048;
                          366
526
542
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          EF-HAND 1.

EF-HAND 2.

EF-HAND 3.

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ANCESTRAL CALCIUM S
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                Thiol protease DOMAIN THIOL PROTEASE DOMAIN
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                                                                                                                                     DOMAIN III,
                                                                                                                DOMAIN IV.
 6E664600B0EFAEBB
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                                                SITE
CRC64
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                                                (POTENTIAL).
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13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG
                                                                  DLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEEWV
DAKQVTYQ-GQRVNLIRMRNPWGEVEWKGPWSDNSYEWNKVDPYEREQLRVKMEDGEFWM
                                                                                                                                     GSGGQQDRPGRWEHRTCRQLL--HLKDQCLISCCVLSPRAGARELGEF------HAFIVS
                                                                                                                                                                                 DGKLVFVHSAQGNEFWSALLEKAYAKVNGSYEALSGGCTSEAFEDFTGGVTEWYDL----
                                                                                                                                                                                                 AGRLCFSRCQREDVFWLPLLEKYYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA
                                                                                                                                                                                                                                             DCWLLAAIASLTLNETILHRVVPYGQS--FQEGYAGIFHFQLWQFGEWVDVVVDDLLPTK
                                                                                                                                                                                                                                                                           DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQEGRWVEVTTDDRLPCL
                                                                                                                                                                                                                                                                                                           LFQDDAFPPVSHSLGFKELG-PNSSKTYGIKWKRPTELLSNPQFIVDGATRTDICQGALG
                                                                                                               -QKAPS-----DLYQIILKALERGSLLGCSINISDIRDLEAITFKNLVRGHAYSVT
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                              17.0%;
31.8%;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 621.5; DB 1
Pred. No. 1.1e-41;
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.10); Mismatches
                                                                                                                                                                                                                                                                                                                                                                               188;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                  363
                                                  336
                                                                                  303
                                                                                                                   277
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Length 713;

15;

9

EMBL; X04366; CAA27881.1; -. EMBL; BC008751; AAH08751.1;

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
CAPNI OR CANPLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86301172; PubMed-3017764;
Aoki K., Imajoh S., Ohno S., Emori Y., Koike M., Kosaki G., Suzuki K.;
"Complete amino acid sequence of the large subunit of the low-Ca2+-
requiring form of human Ca2+-activated neutral protease (muCANP)
deduced from its cDNA sequence.";
SFRDFIREFTKLEICNLTPDALKSRTLRN----WNTTFYEGTWRRGSTAGGCRN---YPA 389
                                    407
                                                                    434
                                                                                                    461
                                                                                                                           ----GRDMETIGFAVYQVPRELAGQPVHLKRDFFLANASRAQSEHFINLREVSNRIRL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel member of the calcium-dependent cysteine protease family.";
Biol. Chem. Hoppe-Seyler 371:171-176(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-90380278; PubMed-2400579;
Sorimachi H., Ohmi S., Emori Y., Kawasaki H., Saido T.C., Ohno S., Minami X., Suzuki K.;
"A novel member of the calcium-dependent cysteine protease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (regulatory) subunit.

SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca++ binding (By similarity).

SIMILARITY: Contains 5 EF-hand calcium-binding domains.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROTEASES.
                               364 ----NPKFWLRVSEPSEV-----YIAVLQRSRLHAADWAGRARALVGDSHTSW
                                                            390 TFWVNPQFKIRLEEVDDADDYDSRESGCSFLLALMQKHR-----RRERRF-----
                                                                                               SPASIPGKHYOAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYD-----REVHLRCEL
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             714 AA.
                                                                                                                                                           SPGYYLAVPSTFLKDAPGEFLLRVFS 487
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red from its cDNA sequence.";
Lett. 205:313-317(1986).
                                                                                                                                                                                                                                                                                                             (Rel. 07, Created)
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SITE 5 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                               SMART; SMOOD4; EPh; 2.

SMART SMOOD4; EF HAND; 2.

PROSITE; PSOOD18; EF HAND; 2.

PROSITE; PSOOD139; THIOL_PROTEASE_CYS; 1.

PROSITE; PSOOG40; THIOL_PROTEASE_ASN; FALSE_NEG.

PROSITE; PSOOG40; THIOL_PROTEASE_ASN; FALSE_NEG.

Hydrolase; Thiol protease; Calcium-binding; Multigene family.

30 220 THIOL PROTEASE DOMAIN I.

THIOL PROTEASE DOMAIN I.

THIOL PROTEASE DOMAIN II.
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1CB6D7C56D063498 CRC64;
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ANCESTRAL CALCIUM
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InterPro; IPR001300; Peptidase_C2.
InterPro; IPR00169; Thiolprot_act_site.
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EF-HAND 2.
EF-HAND 3.
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32.3%; Pred
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Pfam; PF00648; Peptidase_C2; 1.
PRINES, PR00704; CALPAIN.
SMART; SM00030; CYSPC; 1.
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                                                PIR; A26213; CIHUH.
PIR; S10591; S10591.
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MEROPS; C02.001; -.
MIM; 114220; -.
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VARIANTS LGMD2A.

WEDLINE-97294404; PubMed-91:
Richard I., Brenguier L., [
Burqunder J.-M., Chemaly R

"Afranc G., [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95236448; PubMed-7720071; IGND2A.

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P20807; 09Y5S7; 09Y5S6;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 3, Last seguence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94, large [Catalytic] subunit) (Calcium-activated neutral proteinase (CANP 3) (Muscle-specific calcium-activated neutral protease 3 large (CANP 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dickson J.M.J., Love D., Evans C.W.E., "Alternatively exon-spliced isoforms o leukocytes.";
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Sorimachi H., Imajoh-Ohmi S., Emo
Minami Y., Suzuki K.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                    "Juvenile limb-girdle
                                                                                                                                                                                                                                                                             Beckmann J.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVIEW
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                                                                                                                                                                                                                         data
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                                                                                                                                                                                                                       from
     PubMed-9150160;

uier L., Dincer P., Roudaut C., Bady B.,

Chemaly R., Garcia C.A., Halaby G., Jackson

anc G., Legum C., Loiselet J., Merlini L.,
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                                                                                                                                                                                                                                               muscular
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emori Y.,
                                                                                                                                                                                                                                                                                                     Tome
                                                                                                                                                                                                                                                                                             Feingold N., Tome F.M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of calpain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata;
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                                                                                                                                                                                                                                                                                                  Richard
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Arg-1-Xaa with Leu or Val as the P2 residue.

-!- ENZYME REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpastatin.
-!- SUBUNIT: Heterodiner of a large (catalytic) and a small (regulatory) subunit.
-!- SUBUNIT: Heterodiner of a large (catalytic) and a small (regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISUE SPECITICING: 3 ISOFORMS; I (SHOWN HERE), II AND III; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECITICITY: SKELETAL MUSCLE.
-!- DISEASE: DEFECTS IN CAPN3 ARE THE CAUSE OF LIMB-GIRDLE MUSCULAR DYSTROPHY TYPE 2A (LGMD2A). LGMD2A IS BOTH AUTOSOWAL DOMINANTLY AND RECESSIVELY TRANSHITTED. IT IS CHARACTERIZED BY PROGRESSIVE SYMMETRICAL ATROPHY AND WEAKNESS OF THE PROXIMAL LIMB MUSCLES AND ELEVATED SERUM CREATINE KINASE. THE SYMPTOMES USUALLY BEGIN DURING THE FIRST TWO DECADES OF LIFE, AND THE DISEASE GRADUALLY WORSENS, OFTEN RESULTING IN LOSS OF WALKING ABILITY 10 OR 20 YEARS AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT LGMD2A GLY-744.

WEDLINE-98317835; PubMed-9655129;
Penisson-Besnier I., Richard I., Dubas F.,
"Pseudometabolic expression and phenotypic
deficiency in two siblings.";
Muscle Nerve 21:1078-1080(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (8)
VARIANTS LGMD2A ARG-222; GLU-486; TRP-489 AND GLN-/**
MEDLINE-98433925; PubMed-9762961;
Urtasun M., Saenz A., Roudaut C., Poza J.J., Urtizber Cobo A.-M., Richard I., Garcia Bragado F., Leturcq F. Marti Masso J.F., Beckmann J.S., Lopez de Munain A.;
Marti Masso J.F., Beckmann J.S., Lopez de Munain A.;
                                                                                                                                                                                                                                                                                                                                                                                      "Clinical, pathological, and geneticy dystrophy type 2A with new calpain from three Japanese families.", Muscle Nerve 21:1493-1501(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98442618; PubMed-9771675;
Kawai H., Akaike M., Kunishige M.,
Kawajiri M., Nishida Y., Endo I., K
Fujiwara T., Okuno S., Roudaut C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haeffner K., Speer A., Huebner C., Voit T., Oexle K.; A small in-frame deletion within the protease domain specific calpain, p94 causes early-onset limb-girdle m dystrophy 2A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dincer P., Leturcq F., Richard I., Piccolo F., Yalnizoglu de Toma C., Akcoeren Z., Broux O., Deburgrave N., Brengule Roudaut C., Urtizberea J.A., Jung D., Tan E., Jeanpierre M Campbell K.P., Kaplan J.-C., Beckmann J.S., Topaloglu H.; "A blochemical, genetic, and clinical survey of autosomal limb girdle muscular dystrophies in Turkey."; Ann. Neurol. 42:222-229(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT LGMD2A CYS-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98112493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Multiple independent molecular etiology dystrophy type 2A patients from various of Am. J. Hum. Genet. 60:1128-1138(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97410018;
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               SIMILARITY: CONTAINS 4 I SIMILARITY: BELONGS TO I CALPAIN FAMILY OF THIOL
                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Calcium-regulated non-lysosomal thiol-protease CATALYTIC ACTIVITY: Preferential cleavage: Tyr-[-Xaa, Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121:1735-1747(1998).
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93; PubMed-9452114;
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PubMed-9266733;
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variability
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S., Nishino
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DATABASE:

NAME=Leiden

OL PROTEASES. Muscular Dystrophy

pages

ALSO

266

374 473 427 484

713 AA.

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129 CWFLAAIACLTLNQHLLFRVIPHDQS--FIENYAGIFHFQFWRYGEWVDVVIDDCLPTYN 186
                                                                               -----ERWNLKGVA-----GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCC 223
                                                                                                      247 DMYKIMKKAIERGSLMGCSIDDGTNMTYGTSPSGLNMGELIARMVRNM----DNSLLQDS 302
                                                                                                                                             267 RRCWQGLWREGGEGWSQVDAAVASELLSQL-QEGEFWVEEEEFLREFDELTVGYPVTEAG 325
                                                                                                                                                                                                                                                                                                                                                          513 MHGNKQHLQKDFFLYNASKARSKTYINMREVSQRFRLPPSEYVIVPSTYEPHQEGEFILR 572
                                           GVEWNGSWSDRWKDWSFVDKDEKARLQHQVTEDGEFWMSYEDFIYHFTKLEICNLTADA-
                                                                                                                                                                                                                                 326 HLQSLYTERLLCHTRAL-PGAWVKGQSAGGCRNNSGFP----SNPKFWLRVSE----P
                                                                                                                                                                                                                                              SEV----YIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAVGLHLWKV---
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                                                                                                                             224 VLSPRAG - - - - - - - - - - - - ARELGEFHAFIVSDLRELQGQAGQCILLLRIQNPWG
                            133 GRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLA-
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035350; 088666;
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               R MINF 2350U;

R InterPro: IPR0020048; EF-hand.
R InterPro: IPR001300; Peptidase_C2.
R InterPro: IPR001300; Peptidase_C2.
R InterPro: IPR00165; Thiolprot_act_site.
R Ffam; PF001067; Calpain_III; 1.
R Ffam; PF001048; Peptidase_C2; 1.
R PRINTS: PR007046; CALPAIN.
R SMART; SM0024; EFh; 2.
R ROSITE; PS000149; FFh; 2.
R ROSITE; PS000139; THIOL_PROTEASE_CYS; 1.
R ROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
R PROSITE; PS00640; THIOL_PROTEASE_ASN; RALSE_NEG.
R Hydrolase; Thiol Protease; Calcium-binding; Multigene family; Repeat; Multigene family; Repeat; FT DOMAIN 49 234 THIOL PROTEASE DOMAIN II.
FT DOMAIN 429 586 DOMAIN III, C2-LIKE DOMAIN.
FT DOMAIN 125 CALSE DOMAIN III, C2-LIKE DOMAIN.
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KKTKTRIPIEYSDRANSUKELGYDGSSEEGKGKTSPDKQKQ
SPQP -> P (IN ISOFORM II).
MISSING (IN ISOFORM III).
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EF-HAND 1 (PROBABLE).

EF-HAND 2 (PROBABLE).

ANCESTRAL CALCIUM SITE 3 (POTENTIAL).

ANCESTRAL CALCIUM SITE 4 (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.9%; Score blo; 2.3-41;
31.4%; Pred. No. 2.5e-41;
**ive 79; Mismatches 194; Indels 116;
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P -> L (N LGMD2A).

/FTId-vAR_009549.

D -> N (IN LGMD2A).

/FTId-vAR_009550.

S -> F (IN LGMD2A; SEVERE).

/FTId-vAR_009551.
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/FTId=VAR_009552.
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           WWW-"http://www.dmd.nl/capn3_home.html".
 NOTE-Calpain-3 mutations in LGMD2A;
                                                                                                                                                  EMBL; AF127764; AAD28253.1; -. EMBL; AF127765; AAD28254.3; -.
                                                                                                                                     EMBL; X85030; CAA59403.1; -.
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HSSP; P04574; IALV.
MEROPS; C02.004; -.
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ACT_SITE
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Sahr Net. 2, Andrabi S., Peters L.L., Chishti A.H.;

Sahr R.E., Andrabi S., Peters L.L., Chishti A.H.;

"Cloning and characterization of the cDNA and gene encoding the mouse mu-calpain large subunit protein."

"Cloning and characterization of the CDNA and gene encoding the mouse mu-calpain large subunit protein."

"Cloning and characterization of the EMBL/GenBank/DDBJ databases."

"Cloning and the EMBL/GenBank/DDBJ databases."

"Cloring the EMBL/GenBank/DDBJ databases."

"Cloring the EMBL/GenBank/DDBJ databases."

"Cloring the EMBL/GenBank/DDBJ databases."

"Cloring the EMBL/GenBank/DDBJ databases."

"Coractor in Function of Substrates involved in cytoplasmic, Translocates to the plasma

"Cloring and inhibited by calpastatin."

"Cloring and inhibited by calpastatin."

"Cropialatory) subunit."

"Cropialatory) subunit.
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
CAPNI OR CANPI OR CAPAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weiss M.C.,
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CF1;
Polifer C., Poussard S., Faust D.M., Imaizumi-Sherrer T., Ducastaing A., Montarras D., Pinset C., Guenet J.-L.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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19;

CWFLCACAALOKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWYEVTTDDRLPCLA 132

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LFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGOVKQGLLGD 72

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Best Local S
Matches 162
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PROSITE: PS000139; THIOL_PROTEASE_CYS; 1.

PROSITE: PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE: PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
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SMART; SM00230; Cyspc;
SMART; SM00054; EFh; 2
                                                      228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
                                                                                                                                                  114
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InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
                                                                                                                                                             72 DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                                                                                                                                                                                               55
                                                                                                                                                                                                   13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG
                                                                                                                                                                                                                                                      Local Similarity
        GAKQVTYQ.
                   DLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFWV
                                                                                                          AGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                 GSGGQQDRPGRWEHRTCRQLL--+HLKDQCLISCCVLSPRAGARELGEF------HAFIVS
                                                                                           DGKLVFVHSAQGNEFWSALLEKAYAKVNGSYEALSGGCTSEAFEDFTGGVTEWYDL----
                                                                                                                                       DCWLLAAIASLTLNETILHRVVPYGQ-SFQD-GYAGIFHFQLWQFGEWVDVVIDDLLPTK
                                                                                                                                                                                    LFQDEAFPPVSHSLGFKELG-PHSSKTYGIKWKRPTELMSNPQFIVDGATRTDICQGALG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binds
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
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-GQRVNLIRMRNPWGEVEWKGPWSDSSYEWNKVDPYEREQLRVKMEDGEFWM
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                                             --DLYQIILKALERGSLLGCSINISDIRDLEAITFKNLVRGHAYSVT
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                                                                                                                                                                                                                                                     16.9%;
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THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
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ANCESTRAL CALCIUM S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
L -> P (IN REF. 2).
D -> N (IN REF. 2).
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Pred. No. 3.3
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DOMAIN IV.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
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                                                                                                                                                                                                                                                                                               3E1E26C95802B864 CRC64;
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                            DB 1;
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÷ EMBO J.

FUNCTION:

18:6880-6889(1999)

of

basis

enzyme

Calcium-regulated

EVACTION: Calclum-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xa.

cleavage:

Tyr-|-Xaa,

Met-|-Xaa

or

activation.

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                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-20069318; PubMed-10601010;
Hosfield C.M., Elce J.S., Davies P.L., Jia Z.;
"Crystal structure of calpain reveals the structural Ca(2+)-dependent protease activity and a novel mode (
                                                                                                                                                                                                                          MUTAGENESIS OF LYS-230; LYS-234 AND GLU-504. MEDLINE-21269273; PubMed-11102442; Hosfield C.M., Moldoveanu T., Davies P.L., E. "Calpain mutants with increased Ca2+ sensition the role of the C(2)-like domain."; J., Biol. Chem. 276:7404-7407(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q07009;
Q07009;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Calpain 2, large [Catalytic] subunit precursor (EC 3.4. (Calcium-activated neutral proteinase) (CANP) (M-type)
                                                                                                                                                         mutagenesis."
                                                                                                                                          FEBS Lett. 368:397-400(1995).
                                                                                                                                                                  Arthur J.S., Gauthier S., Elce J.S.; "Active site residues in m-calpain:
                                                                                                                                                                                          MUTAGENESIS OF CYS-105; HIS-262; MEDLINE-95361909; PubMed-7635186;
                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE.
MEDLINE=21240297; PubMed=11342050;
Moldoveanu T., Hosfield C.M., Jia Z.,
Moldoveanu T., Structural changes in
                                                                                                                                                                                                                                                                                                                                                                                                                 Deluca C.I., Davies P.L., Samis J.A., Elce "Molecular cloning and bacterial expression II 80 kDa subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             "Ca(2+)-induced structural changes partial proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=94032492;
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                                                                                                                                                                                                                                                                                                                                                                                                         Biochim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8218419;
es P.L., Samis J.A.,
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                                 identification
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01 ALGDCWLLAAIASLTLNEEILARVVPLDQS--FQENYAGIFHFQFWQYGEWVEVVVDDRL 158
                                                                                                                                                                   189 GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARE-----LGEFHAFIV 242
                                                                                                                                                                                                                                                          42 AGALFQDPSFPALPSSLGFKELG-PYSSKTRGIEWKRPTEICADPQFIIGGATRTDICQG 100
                                                     69 LLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128
                                                                                                                                        129 PCLAGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                         326 MSFSDFLRHYSRL-----EICNLTPDTLTCDSYKKWKLTKMDGNWRRGSTAGGCR 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 N-NSGFPSNPKFWLRVSEPSE----VYIAVLQRSRLHAADWAGRARALVGDSHT
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Arg-1-Xaa with Leu or Val as the P2 residue.
COFACTOR: Binds 3 calcium ions.
ENZYME REGULATION: Activated by 200-1000 micromolar concentrations
of calcium and inhibited by calpastatin.
SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ydrolase; Thiol protease; Calcium-binding; Repeat; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DECREASE OF 12% OF THE ACTIVITY
                                                                                                                                                 membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO EFFECT.
DECREASE OF 84% OF THE ACTIVITY
DECREASE OF 85% OF THE ACTIVITY
DECREASE OF 20% OF THE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECREASE OF 95% OF THE ACTIVITY DECREASE OF 10% OF THE ACTIVITY
                                                                                                         (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANCHORS TO THE SMALL SUBDNIT CALPAIN 2, LARGE (CATALYTIC); THIOL PROTEASE DOMAIN I. THIOL PROTEASE DOMAIN II. DOMAIN III, C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296B0DC3BEEF5B90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00018: EF HAND: 2.
PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE: PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE: PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCESTRAL CALCIUM
ANCESTRAL CALCIUM
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InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00036; calpain_III; 1.
Pfam; PF00048; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CySPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
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K-VE:
H-VS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L09120; AAA16327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S38361; S38361.
PDB; 1DF0; 21-JUN-00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C02.002;
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MUTAGEN
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CAN3_MOUSE STANDARD; PRT; 821 AA.
064601; 09WUC5;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2101 (Rel. 40, Last annotation update)
18-CCT-2101 (Rel. 40, Last annotation update)
19-CCT-2101 (Rel. 40, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (SHORT ISOFORM).
Dickson J.M.J., Love D., Evans C.W.E.;
"Alternatively exon-spliced calpain 3 isoform expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richard I., Beckmann J.S.; "Molecular cloning of mouse canp3, the gene associated with limb-girdle muscular dystrophy 2A in human."; Manm. Genome 7:377-379(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96269607; Pubmed=8661728
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74; Gaps

16.8%; Score 614; DB 1; Length 700; 30.8%; Pred. No. 4.3e-41; .ive 78; Mismatches 205; Indels 7;

Best\_Local Similarity 30.8 Matches 159; Conservative

Similarity

**Ouery Match** 

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Best Local Similarity 29.9
Matches 167; Conservative
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Pfam; PF00036; efhand; 3.
Pfam; PF000648; Peptidase C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
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CA_BIND
DOMAIN
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VARSPLIC
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ACT_SITE
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DOMAIN
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PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189
                                              187
                                                                   133
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InterPro; IPR000169; Thiolprot_act
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                                                                                        129
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                                                                                                                                                                                                                                                                                                                                                                                      lternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch]
                                                                                                                        LFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLGD
DMYKIMRKAIERGSLMGCSIDDGTNMTYGTSPSGLNMGELIARMVRNMDNSLLRDSDLDP
                                                     CWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCLA 132
                                         NQLVFTKSNHRNEFWSALLEKAYAKLHGSYEALKGGNTTEAMEDFTGGVTEFFEIKDAPS
                                                                                CWFLAAIACLTLNERLLFRVIPHDQS--FTENYAGIFHFQFWRYGDWVDVVIDDCLPTYN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT:
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                                                                                                                                                                                                                                                                                                                                                                           splicing.
                                                                                                                                                                                                                                                                                                                                                                                                  Thiol
                                                                                                                                                                                                                            821 AA;
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429
587
650
705
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735
730
800
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334
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268
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586
649
820
716
746
781
781
129
334
315
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                                                                                                                                                                     16.6%; Score 605.5; DB 1
29.9%; Pred. No. 2.5e-40;
Live 83; Mismatches 174
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                                                                                                                                                                                                                      EF-HAND 1 (PROBABLE).
EF-HAND 2 (PROBABLE).
ANCESTRAL CALCIUM SITE 3 (PO ANCESTRAL CALCIUM SITE 4 (PO BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY ISOFORM).
MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                   THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                 DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                             LINKER.
                        GVAGSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its content
                                                                                                                                                                                         Length
                                                                                                                                                                    Indels 135;
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                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            family; Repeat;
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                     194
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500
560 TYEPHQEGEFILRVFSEKR 578
                             472 TFLKDAPGEFLLRVFSTGR
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                                                         FT IGFAIYEVPKEMHGNKQHLQKDFFLYNASKARSKTYINMREVSQRFRLPPSEYVIVPS
                                                                                      QAVGLHLWKV-----EKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPS
                                                                                                                                                     WLRV-----SEPSEV----YIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHY
                                                                                                                                                                                    TKLEICNLTADA-----LESDKLQTWTVSVNEGRWVRGCSAGGCRN---FPDTFWTNPQY
                                                                                                                           RLKLLEEDDDPEDSEVICSFLVALMQKNR---
                                                                                                                                                                                                      DELTYGYPYTEAGHLQSLYTERLLCHTRAL-PGAWYKGQSAGGCRNNSGFP----SNPKF
                                                                                                                                                                                                                                               EKVKLVRLRNPWGQVEWNGSWSDGWKDWSFVDKDEKARLQHQVTEDGEFWMSYDDFVYHF
                                                                                                                                                                                                                                                                      RGSDDRPS
                                                                                                                                                                                                                                                                                                                                             -GQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAFIVSDLRELQGQAG
                                                                                                                                                                                                                                                                                                                    -RTIVPVQYETRMAC----
                               ₹ 490
                                                                                                                            ----RKDRKL-
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                                                                                                                         -----GANL
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RESULT
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                                                                                            MEDLINE=89166474; PubMed=2852952;
MEDLINE=89166474; Ohno S., Emori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _HUMAN
"Molecular cloning of the cDNA for the large subunit of high-Ca2+-requiring form of human Ca2+-activated neutral biochemistry 27:8122-8128(1988).
                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                     (Millimolar-calpain). CAPN2 OR CANPL2.
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                         form of human Ca2+-activated neutral protease.";
                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                ¥.,
                                                                                                          Kawasaki Hî, Sugihara
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Nakagawa K:, Irie A., Sorimachi H., Bourenkow G. X., Marunik H., Suzuki K., Bode W.;

"The crystal structure of calcium-free human m-calpain suggests an electrostatic switch mechanism for activation by calcium.",

Proc. Natl. Acad. Sci. U.S.A. 97:588-592(2000).

-I-FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Afg-|-Xaa with Leu or Val as the P2 residue.

-i- COFACTOR: Binds 3 calcium ions.

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MEDLINE=20105516; PubMed=10639123; Strobl S., Fernandez-Catalan C., Braun M., Hub. Nakagawa K., Irie A., Sorimachi H., Bourenkow

Huber R., kow G., Bar

Masumoto H.,

X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).

Hata A., Ohno S., Akita Y., Suzuki K.; "Tandemly reiterated negative enhancer-like transcription of a human gene for the large dependent protease.";
J. Biol. Chem. 264:6404-6411(1989).

elements regulate subunit of calcium

TISSUE-Lymph node; MEDLINE-89197947; PubMed-2539381; SEQUENCE OF 1-79 FROM N.A.

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CAN3_RAT
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
ENZYME REGULATION: Activated by 200-1000 micromolar concentrations of calcium and inhibited by calpastatin.
SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANCHORS TO THE SMALL SUBUNIT (POTENTIAL). CALPAIN 2, LARGE [CATALYTIC] SUBUNIT.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00067; Calpain_III; 1.
Pfam; PF00068; efhand; 3.
Pfam; PF00068; Peptidase_C2; 1.
PRINTS; PR000704; Calpain.
SMART; SM000230; CysPc; 1.
SMART; SM00030; CysPc; 1.
SMART; SM00018; EF_HAND; 2.
PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS00019; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00040; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
PAGASITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                             membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                       (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> G (IN REF. 2).

R -> IE (IN REF. 2).

A944D13BC8465531 CRC64;
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ANCESTRAL CALCIUM
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BY SIMILARITY.
BY SIMILARITY.
S -> G (IN REF
MR -> IE (IN R
                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Peptidase_C2.
InterPro; IPR000169; Thiolprot_act_site.
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EF-HAND 2.
EF-HAND 3.
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                                                                                                 CALPAIN FAMILY OF THIOL PROTEASES.
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80006 MW;
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700
335
335
514
529
700
552
596
661
691
105
286
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PDB; IKFU: 07-DEC-01
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73
700 AA;
                                                                                                                                                                                                                                                                         MEROPS; C02.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure
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15;
                                                                                                                  69 LLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128
                                                                                                                                                  129 PCLAGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                              Gaps
                                                     68
                                                10 ARELFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQG
                           74;
   Length 700;
             Pred. No. 2.6e-40;
76; Mismatches 209; Indels
  ; DB 1;
2.6e-40;
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16.6%; Score 604; 30.4%; Pred. No. 2
                          Conservative
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Matches 157;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                      267 TGAEEVESN-GSLOKLIRIRNPWGEVEWTGRWNDNCPSWNTIDPEERERLTRRHEDGEFW 325
                                                                                                                                                                                                                        VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHT-----RALPGAWVKGQSAGGCR 356
                                                                                                                                                                                                                                                                           N-NSGFPSNPKFWLRVSEPSE------VYIAVLQRSRLHAADWAGRARALVGDSHT 405
                                                                                                                                                                                                                                                                                                                                                        -SWSPASIPGKHYQAVGLHLWK----VEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCE 460
                                                                                                                                                                                                                                                                                                                                                                                                   -----REVLNRFK 476
PTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELK 218
                                                                          -----KPPPNLFKIIQKA--LQKGSLLGCSIDITSAADSEAITFQKLVKGHAYSV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94, large (catalytic) subunit) (Calcium-activated neutral proteinase 3) (CANP 3) (Muscle-specific calcium-activated neutral protease 3 large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 254:20106-20111(1989).
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease.
-!- CATALIYIT CACIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.
-!- ENZYME REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpastatin.
-!- SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90062125; PubMed-2555341; Sorimachi H., Imajoh-Ohmi S., Emori Y., Kawasaki H., Ohno S., Minami Y., Suzuki K.; Minami Y., Suzuki K.; Molecular cloning of a novel mammalian calcium-dependent protease distinct from both m- and mu-types. Specific expression of the mRNA
                                                                                                                                                                                                                                                                                                  189 GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEF----HAFIV
                                                                                                                 243 SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW
                                                                                                                                                                                                                                                                                                                                                                                             429 IGFGIYEVPEELSGQTNIHLSKNFFLTNRARERSDTFINL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 LSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Skeletal muscle;
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as

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SMART; SM0023v, SMART; SM0023v, SMART; SM00054; EFh; 2.

R PROSITE; PS00018; EF_HAND; 2.

R PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

DR PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

DR PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

RW Hydrolase; Thiol protease; Calcium-binding; Multigene family; YOMAIN 234 THIOL PROTEASE DOMAIN II.

YOMAIN 235 428 THIOL PROTEASE DOMAIN II.

DMAIN II.

SOMAIN II.

OMAIN III, C2-LIKE DOMAIN.
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Matches 170
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InterPro; IPR001300; PeptIdase_C2.
InterPro; IPR001309; Thiolprot_act_site.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF000648; PeptIdase_C2; 1.
Pfam; PF00648; PaptIdase_C2; 1.
PRINTS; PR00704; CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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        PDDSEVICSFLVALMQKNR-
                                                                                        EAGHLQSLYTERLLCHTRAL-PGAWVKGQSAGGCRNNSGFP----SNPKFWLRVSE----
                                                                                                                                                                  PWGRRCWQGLWREGGEGWSQVDAAVASELLSQL-QEGEFWVEEEEFLREFDELTVGYPVT
                                                                                                                                                                                                    RDSDLDPRASDDRPSRTIVPVQYETRMACGLVKGHAYSVTGLEEALFK-GEKVKLVRLRN
                                                                                                                                                                                                                                                                                                                                                     LYLDPEFPPDETSLFYSQKFPI-QF----VWKRPPEICENPRFIIGGANRTDICQGDLGD
                                    --PSEV----YIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAVGLHLWKV
                                                                                                                                                                                                                                          SCCVLSPRAG
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                                                                                                                                                                                                                                                                                                                                                                                                    CWLLAAIACLTLNERLLFRVIPHDQS--FTENYAGIFHFQFWRYGDWVDVVIDDCLPTYN
                                                                                                                                                                                                                                                                                                                                                                                                                            CWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCLA 132
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31.0%;
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EF-HAND 1 (PROBABLE).

EF-HAND 2 (PROBABLE).

ANCESTRAL CALCIUM SITE 3 (
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BY SIMILARITY.
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Pred. No. 7.
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      GANLFTIGFAIYEV
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RESULT 13
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ID CAN2_C
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CAN2_CHICK STANDARD; PRT; 700 AA.
092178;
092178;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millimolar-calpain).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle expresses four distinct calpains.";
Blochim. Biophys. Acta 1261:381-393(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95260862; PubMed=7742367;
Sorimachi H., Tsukahara T., Okada-Ban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Identification of a third ubiquitous calpain species --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 ILRVFSEKR 578
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                                                                                                                                                                     CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa or Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concentrations of calcium and inhibited by calpastatin.

SUBUNIT: Heterodimer of a large (catalytic) and a small
                      (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS SIMILARITY: BELONGS TO PERTIDASE FAMILY C2; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                    FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity). CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa
CALPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLRVFSTGR
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Pfam; PF01067; Calpain\_III; Pfam; PF00036; efhand; 3. Pfam; PF00648; Peptidase\_C2; PFINTS; PR00704; CALPAIN. use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See l or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its two by non-profit institutions as long as its content is in no way SMART; EMBL; D38026; BAA07228.1; HSSP; P17655; 1DKV. InterPro; IPR001300; InterPro; IPR000169; InterPro; IPR002048; MEROPS; SM00230; CysPc; SM00054; EFh; 2 C02.002; PS00139; THIOL\_PROTEASE\_CYS; EF\_HAND; license agreement (See http://www.isb-sib. Peptidase\_C2. Thiolprot\_act\_site. EF-hand ۲ Usage and for

us-09-768-877-2.sep19.rsp

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
              gallus (Chicken).
                                                   NCBI_TaxID=9031;
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      17;
PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
Hydrolase; Thiol protease; Calcium-binding; Multigene family.
PROPEP 1 1 9 ANCHORS TO THE SMALL SUBUNIT (POTENTIAL).
CHAIN 20 700 CALPAIN 2, LARGE [CATALXTIC] SUBUNIT.
DOMAIN 20 THIOL PROTEASE DOMAIN II.
DOMAIN 355 514 DOMAIN III, C2-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 SAGGCRN-NSGFPSNPKFWLRVSEPSE-----VYIAVLORSRLHAADWAGRARAL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 GEDMHTIGFALYEVPPEFSGOTNIHLSKNFFLTNKAREKSNTFINL------RE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                  40 LQGGR-----LFHDPSFPAGPAALGYRELGPNSYKTKGVVWCRPTELCSCPRFIAGGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
18-Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94, large [catalytic] subunit (Calcium-activated neutral proteinase 3)
(CANP 3) (Muscle-specific calcium-activated neutral protease 3 large
                                                                                                                                                                                                                                            9
                                                                                                                            4 (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 121 EVTTDDRIPCLAGRICESRCQREDVFWLPLLERVYAKVHGSYEHLWAGQVADALVDLTGG
                                                                                                                                                                                                                                                                                                                                                                                         233 ELGEFHAFIVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASEL
                                                                                                                                                                                                                                                                                                                                                                                                                              293 LSQLQEGEFWVEEEEFLREFDELTVG--TPVTEAGHLQSLYTERLLCHTRALPGAWVKGQ
                                                                                                                                                                                                                                                                             61 REGOVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV
                                                                                                                                                                                                                                                                                                                            21 IAEMYEL-----QKAPPNLF-----KIIQKALQKGSLIGGCSIDITSAAETEAVTSQ
                                                                                                                                                                                                                                                                                                                                                                                                      400 VGDSHT-SWSPASIPGKHYQAVGLHLWK----VEKRRVNLPRVLSMPPVAGTACHAYDRE
                                                                                                                                                                                                                                        1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
                                                                                                                                                                                                                                                                                                                                                      LAERWNIKGVAGSGGQQDRPGRWEHRTCRQLLH--LKDQCLISCCVLSPRAG-----AR
                                                                                                                                                                                                                        75;
                                                                                                                                                                                                 16.4%; Score 597.5; DB 1; Length 700; 31.2%; Pred. No. 8.7e-40; live 81; Mismatches 203; Indels 75
                                                                                                                                                                        C3AEDB39CCB56D3B CRC64;
                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 VHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANCESTRAL CALCIUM
ANCESTRAL CALCIUM
                                                                                                                                             SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 AA.
                                                                                              EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
                                                                                      DOMAIN IV.
                                                                                                                                                                         MW.
                                                                                                                                                                         79228
                                                                                                                                                                                                                     Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                210
351
351
352
700
552
552
652
651
105
                                                                                                                                 680 69
105 14
262 2
286 2
                                                                                                                                                                                                            Local Similarity
                                      20
20
211
356
515
530
541
585
615
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092177;
                                                                                                                                           ACT_SITE
ACT_SITE
                                                                                                                                                             ACT_SITE
SEQUENCE
                                                                                                                                                                                                    Query Match
                                                                                                     CA_BIND
CA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Subunit)
                                                                                             CA_BIND
                                                                           DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                       181
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CAN3_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                             ö
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                (regulatory) subunit.
-:- SUBCELLUIAR LOCATION: Cytoplasmic and nuclear (Potential).
-:- TISSUE SPECIFICITY: SKELETAL MUSCLE. LOW LEVELS IN SPLEEN,
INTESTINE AND BONE.
-:- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN AS THE CALPAIN FAMILY OF THIOL PROFEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANCESTRAL CALCIUM SITE 3 (POTENTIAL)
ANCESTRAL CALCIUM SITE 4 (POTENTIAL)
                                                                   Suzuki K.; "Identification of a third ubiquitous calpain species -- chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MENCHE'S CULLIUM;

InterPro; IPR001300; Peptidase_C2.

InterPro; IPR001300; Peptidase_C2.

InterPro; IPR001169; Thiolprot_act_site.

R InterPro; Calpain_III; 1.

R Pfam; PF01067; Calpain_III; 1.

R Pfam; PF000648; Peptidase_C2; 1.

R PRINTS; PR00704; CALPAIN.

R PRINTS; SM00130; CySPC; 1.

SMART; SM00130; CySPC; 1.

R PROSTIE: PS0018; EF HAND; 2.

R PROSTIE: PS0018; EF HAND; 2.

R PROSTIE: PS00640; THIOL_PROTEASE_HS; FALSE_NEG.

R PROSTIE: PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

HYdrolase: Thiol protease; Calcium-binding; Nuclear protein;
                                              Sorimachi H., Tsukahara T., Okada-Ban M., Sugita H., Ishiura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAIN.
DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
E8DE99411C51041E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF-HAND 1 (PROBABLE).
EF-HAND 2 (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 589.5; DB 1;
28.6%; Pred. No. 4.5e-39;
tive 87; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
TISSUE=Lung;
MEDLINE=95260862; PubMed=7742367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D38028; BAA07230.1; -. HSSP; P04574; 1ALV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
351
810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; C02.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family
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580
639
694
724
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Best Local Simi
Matches 161;
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SEQUENCE
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RESULT
CAN_DRC
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                                                                                                                                                                                                                                                                                                                                                                                                                DROME
                                                                                                                                                                                                                                                                                                             Q11002; Q9V8U7;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calpain (EC 3.4.22.17) (Calcium-activated neutral proteinase)
CALPA OR CG7563.
                                                                                                                                       Emori Y., Saigo K.;
"Calpain localization changes in cytoskeletal changes during early
                                                                                                                                                                                 STRAIN=CANTON-S;
MEDLINE=95014293; PubMed=7929201;
                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                              Theopold U., Pinter M., Nassel D.R., Hultmark D.
                                                                          STRAIN-CANTON-S
                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                CAN_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553
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                                                                                                                 Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELKDAPGEFLIRVFSTGRVSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMRLVRLRNPWGQVEWNGPWSDKSEEWNFIDEEEKIRLQHKIAEDGEFWISLEDFMRHFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYEPHQEGEFILRVFSEKR-SLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEDDDPEDEEVICSFLVALMQKNR-----RKERKLGANLYTIGFAIYEVPKEMHGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLEICNLTPD----TLEADKLQTWTVSVNEGRWVRGCSAGGCRNYPDTFWTNPQYRLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTYGYPYTEAGHLQSLYTERLLCHTRAL-PGAWYKGQSAGGCRN-NSGFPSNPKFWLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQL-QEGEFWVEEEEFLREFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTDERPA-W-----TIMPMQYETRMSC------GLVKGHAYSVTAVEETT-YKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAFIVSDLRELQGQAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIYKIMKHAIARGSLMASSIDDNLGFHYGAAPRSDIGELIARMVKNLENAQMTYSTVDYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CWFLAAIACLTLNKKLLCRVIPHDQS--FIQNYAGIFHFQFWRYGDWVDVIIDDCLPTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCLA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYEDPDFPPNETSLFYSQKVPI----KFEWKRPREICENPRFIIGGANRTDICQGELGD
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a Drosophila calpain homolog specifically st of nerve, midgut, and blood cells.";
                                                                                                             269:25137-25142(1994).
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                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                         PubMed=7823949;
er M., Daffre S.,
                                                                                   CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GVAGSG---
                                                                                                                                        early
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                                                                                                                                                     coordination with actin-related
                                                                                                                                        embryonic
                                     Tryselius Y., Friedrich P.,
                                                                                                                                                                                                                                                                                                                                                                                              828
                                                                                     AND
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                                                                                  ALTERNATIVE SPLICING
                                                                                                                                       development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REISERFRLPPSEYVIIPS
              expressed in
                                                                                                                                                                                                                                                                  Muscomorpha;
                                                                                                                                                                                                                                                                                                                       (CANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
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EMBL; X78555; CAA55298.1; EMBL; X78555; CAA55297.1; EMBL; Z46891; CAA86993.1; EMBL; Z46892; CAA86994.1;

ALT\_INIT

P17655;

1DKV

AE003796; AAF57563.1;

or send

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AN ANTIL J. Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G., An Alril J.F., Apjayani A., Darter E.G., Helt G., Nelson C.R., Badvin D., An Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bebson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ethick R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dender C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dender C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dender C., Gebart H. M., Glasser K., Ra Goldek A., Gong F., Gorrell J.H., Gu Z., Gebbart M.M., Glasser K., Ra Goldek A., Gong F., Gorrell J.H., Gu Z., Gebbart M.M., Glasser K., Ra Goldek A., Gong F., Gorrell J.H., Gu Z., Gebbart M.M., Glasser K., Ra Harris M.L., Harvey D., Helman T.J., Wel M.H., Ibeywam C., Ra Hostin D., Houston K.A., Howland T.J., Wel M.H., Ibeywam C., Ra Hostin D., Houston K., Karfet C., Kravitz S., Kulp D., Lai Z., Ra Hould J., Ra Hould T.J., Wel M.H., Ibeywam C., Ra McInder B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Hould S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Hould S.M., McIntosh T.C., McLeod M.P., McPherson D., Ra McIntosh T.C., McLeod M.P., McPherson D.L., Ra Hould S.M., Murphy B., Murphy L., Murphy D.M., Nelson D.L., Ra Hould S.M., McIntosh T.C., Scheeler F., Shah H., Ra Melson D.R., Nelson K., Sunders R.D. C., Scheeler F., Shah T., Ra Palazzolo M., Stingson M., Stupski M.P., Shah H., Ra Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Shah T., Ra Shue B.C., Stapleton M., Strong R., Sun E., Ra Zheng X.H., Wassarman D.A., Weinstock G.M., Welssenbach J., Ra Zheng X.H., Wassarman D.A., Weinstock G.M., Welssenbach J., Walley S., Kulp J., Walley S., Yao Q., Zheng L., Wassarman D.A., Weinstock G.M., Welssenbach J., Walley S., Walley S., Walley S., Walley S
                                                      between the Swiss Institute. There are the European Bioinformatics Institute. There are the European Bioinformatics Institute. There are the the European Bioinformatics Institute. There are the the European Bioinformatics Institute. There are the European Bioinformatics Institute. 
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MISCELLANEOUS: THIS PROTEIN BINDS CALCIUM.
SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALPAIN FAMILY OF THIOL PROTEASES
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an email to license@isb-sib.ch).
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ANCESTRAL CALCIUM SITE 3 (POTENTIAL)
ANCESTRAL CALCIUM SITE 4 (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
      R InterPro; IPR002048; Er-hand.
R InterPro; IPR001309; Peptidase_C2.
R InterPro; IPR001309; Peptidase_C2.
R InterPro; IPR00169; Thiolprot_act_site.
R Pfam; PF00164; Calpain_III; 1.
R Pfam; PF00048; Peptidase_C2; 1.
R Pfam; PR00030; Cyspe; 1.
R PRINTS; PR00704; EFP, 2.
R PRNST; SN00230; Cyspe; 1.
R SMART; SN00139; THIOL_PROTEASE_CYS; 1.
R PROSITE; PS00139; THIOL_PROTEASE_RIS; FALSE_NEG.
R PROSITE; PS00639; THIOL_PROTEASE_ASN; FALSE_NEG.
R PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
R PROMAIN ERROR.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
ENDDH -> RTSKQ (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAIN.
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09576D1268BD569C CRC64;
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EF-HAND 1 (PROBABLE).
EF-HAND 2 (PROBABLE).
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   FlyBase; FBgn0012051; CalpA
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306
397
828 AA;
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22;
                                                                                                    LLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128
                                                                                                                                                                               PCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                                                                                                                                                                                                                                                    257 EAPGNLFTILQKAAERNSMMGCSIEPDPNVTEAETPQGLIRGHAYSITKVCLID----- 310
                                                                                                                                                                                                                                                                                                                                                                                                         311 -----IVPPNR--QGK----IPMIRWRNPWGNEAEWNGPWSDSSPEWRYIPEEQKAE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 L-LSQLQEGEFWVEEEEFLREFDELTV----GYPVTE----AGHLQ---SLYTERLLCHT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |: ::||||: ::|| || : : :|| 357 IGLTFDRDGEFWASPQDFLNHFDRVEICNLSPDSLTEDQQNSGKRKWEMSMY------ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 DWAGRARALVGDSHTSWSPASIPGKHYQAVGLHLWKVEKRRV-NLPRVLSM---PPVAGT 446
                                                                                                                                                                                                                                                                                                            ----GGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGAR 232
                                                                                                                                                                                                                                                                                                                                                                                   233 ELGEFHAFIVSDLRELQGQAGQCILLLRIQNPWGRRC-WQGLWREGGEGWSQVDAAVASE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RALPGAWVKGQSAGGCRN-NSGFPSNPKFWLRVSEPSE-----VYIAVLQRSRLHAA 390
Query Match
16.1%; Score 586; DB 1; Length 828;
Best Local Similarity 30.3%; Pred. No. 8.8e-39;
Matches 167; Conservative 83; Mismatches 185; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---EGEWIPGVTAGGCRNFLDTFWHNPQYIITLVDPDEEDEEGGCTVIVALMQKNR---- 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 ACHAYD-REVHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLS-----AIRAV 499
                                                                          LFRDAAFPAADSSLFCDLSTPLAQF--RED--ITWRRPQEICATPRLFPDDPREGQVKQG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RSKRNM------GMECLTIGFAIYSLNDRELENRPQGLNFFRYKSSVGR
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OY 500 AKNTTPGAALP 510

565 ADTITPGFPTP 575

Search completed: September 19, 2002, 14:54:24 Job time: 263 sec



OM protein - protein	search,	using sw model	٠.
Run on:	September 19,	2002, 14:48:56; Search (without 3010.351	time 21.45 Seconds alignments) Million cell updates/sec
Title: Perfect score: Sequence:	US-09-768-877-2 3649 1 MRAGRGATPARELFRDAAFP		SQEMIGQFIQEVSYMAVMKT 672
Scoring table:	BLOSUM62 Gapop 10.0 ,	Gapext 0.5	
Searched:	283138 seqs,	96089334 residues	
Total number of h	hits satisfying	ng chosen parameters:	283138
Minimum DB seq le Maximum DB seq le	length: 0 length: 2000000000	0000	
Post-processing:	Minimum Match Maximum Match Listing first	1 0% 1 100% 1 45 summaries	
Database : 1 2 3	PIR_71:* : pir1:* : pir2:* : pir3:* : pir4:*		
Pred. No. is to score greater and is derived	the number than or ec l by analys	esults predicted he to the score of the total score	y chance to have a ne result being printed, distribution.
	erv	SUMMARIES	
No. Score Ma	Query Match Length D	B ID	Description
<b>₩</b> ₩₩₩	17.6 705 16.9 714 16.9 821 16.8 700 16.8 703 16.7 700		calpain (EC 3.4.22 calpain (EC 3.4.22 calpain (EC 3.4.22 calpain (EC 3.4.22 calpain (EC 3.4.22
597.5 589.5	.4 821 .4 700 .2 810	1 B34488 2 S57194 1 S57196 1 A55054	(EC 3.4 (EC 3.4
569.5 569.5	.6 647		calpain (EC 3.4.22 C06G4.2 protein - tissue-specific ca
540 506.5	. 8 758		erminin (EC 3.
457.5 376.5	.5 2143		ypotnetic
376.5 335.5	.3 1597 .2 616		sor protein, large gene small optic l
326 271.5	.9 634		hypothetical prote hypothetical prote
191.5 189.5	.4 422 .2 1134 .2 617		σω
25 162.5 4 26 120.5 3 27 114 3	.5 623 .3 217 .1 499		
111	.0 757 .0 3519		subtilisin-type pr polyketide synthas

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В Ş

Query Match Best Local Similarity

17.6%; 32.0%;

Matches 162;

Conservative

78;

Score 642; DB 1; Length 705; Pred. No. 2.1e-42; B; M1smatches 188; Indels

78;

Gaps

16;

	45	44	43	42	41	40	39	88	3/	5 6		) L	ى ر • ر		ىد د	31	30	
	99.5	99.5	100.5	101	101.5	101.5	102	102	102.5	102.5	TO2.5	104.5	100	u (	106	107	107	
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	S48719	JC5119	A53210	AH1852	AI1941	A24815	A57788	JC4335	A82822	A39045	I55593	T00328	0896TS	000/09	70000	T35599	G84888	
•	phospholipase-A(2)	anti-mullerian bor	phospholipase A2 r	hypothetical prote	hypothetical prote	calpain (EC 3.4.22	fatty-acid synthas	anti-mullerian hor	NADH-ubiquinone ox	protein-glutamine	connexin 37 - huma	hypothetical prote	protein-glutamine	brain-specific ser	ביסטמטום טאא וופרווץ	probable DNA mother	probable transketo	

## ALIGNMENTS

F;533-564/Domain: calmodulin repeat homology <EF1>
F;576-608/Domain: calmodulin repeat homology <EF2>
F;676-608/Domain: calmodulin repeat homology <EF3>
F;609-638/Domain: calmodulin repeat homology <EF4>
F;641-673/Domain: calmodulin repeat homology <EF4>
F;674-705/Domain: calmodulin repeat homology <EF5>
F;2/Modified site: blocked amino end (Met) (in mature) (Met) (in mature) (Met) A;Cross-references: EMBL:X01415; NID:g63332; PIDN:CAA25658.1; PID:g63333
R;Emori, Y.; Ohno, S.; Tobita, M.; Suzuki, K.
FEBS Lett. 194, 249-252; 1949-258.
A;Reference number: A91354; MUID:86082358
A;Contents: annotation; gene structure
C;Comment: This calpain has calcium requirements intermediate between those of the A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic d. (Keywords: blocked amino end; calcium binding; cysteine proteinase; duplication; E;78-330/Domain: calpain catalytic domain homology <CALP> A;Introns: 82/3; 106/1; 145/3; 190/2; 246/3; 274/3; 303/2; 328/2; 382/1; 438/3; 442 C;Complex: heterodimer of L (large) and S (small) chains A:Description: catalyzes the hydolysis of peptides C; Function: A; Molecule type: mRNA A; Residues: 1-705 <OHN> A;Title: Evolutionary origin of a calcium-dependent protease by fusion of genes for A;Reference number: A93348; MUID:85061606
A;Accession: A00979 calpain (EC 3.4.22.17) large chain 4 - chicken
NALITERIAN CALANTIC CHAIN; intermediate calcium activated neutral
C:Species: Gallus gallus (chicken)
C:Date: 17-May-1985 #sequence\_revision 09-Aug-1997 #text\_change 24-Nov-1999
C:Accession: A00979 R;Ohno, S.; Emori, Nature 312, 566-57 Genetics: Emori, Y.; Imajoh, S.; Kawasaki, H.; Kisaragi, M.; Suzuki, 566-570, 1984 (in mature form) #status experimental
status predicted 7

Db 165 DGELLFVHSAECTEFWSALLERAYAKLNGCYESLSGGSTTEGFEDFTGGVAEMYDLK 221	F:618-647/Domain: calmodulin repeat homology <ef3></ef3>
OY 192 GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF 240	homology <ef5></ef5>
Db 222RAPRNMGHIRKALERGSLLGCSIDITSAFDMEAVTFKKLVKGHAY 267	F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental F:115,272,296/Active site: Cys, His, Asn #status predicted
OY 241 IVSDLRELQCQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQE 298	
Db 268 SVTAFKDVNYRGQQEQLIRIRNPWGQVEWTGANSDGSSEWDNIDPSDREELQLKWED 324	Query Match 16.9%; Score 618.5; DB 1; Length 714; Best Local Similarity 32.3%; Pred. No. 1.5e-40;
Qy 299 GEFWVEEEEFLREFDELTVGYPVTEACHLOSLYTERL-LCHTRALPGAWVKGOSAGGCRN 357	les 166; Conservative 7
325 GEFWASFRDFWREFSRLEICNLTPDALTKDELSRWHTOVFEGTWRRGSTAGGCRN	QY 13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG 71
N-SGPPSNPKFWI.RVSPPSFVVTAVIAVIAPSBI.HAMGAGDAMASVIACHCHA.	EAFPPVPQSLGYKDLG-PNSSKTYGIK
380 NPATFWINPOFKIKLLEEDDDPGDDEVACSFLVALWQXHRRRERRVGGDMHTI	Gy 72 DCWFLCACAALQKSRHLLDQVIPPGQPSWADQBTRGSFTCRIWQFGRWVEVTTDDRLPCL 131
	TLNDTLLHRVVPHGQSFQNGYAGIFHE
:: :  :  : :      : : :         : : :         : : :         : :         : : :         : :           : :           : :	QY 132 AGRLCESRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
487	SGGSTSEGFEDE
:	OY 192 GSGGQORPGRWEHRTCRQLLHLKDQCLISCCVLSPRA-GARELGEFHAFIVSDL 245
RESULT 2	246 RELOGOAGOCILLIRIONPWGRRCHOGLWREGGEGGGSOUDANASELISOLOEGEFWVER
IHUH alpain (EC 3.4.22.17) large chain 1	280 KOV-NYRGOVYSLI PRARNPAGRAVEMENTA SEMINANDEVERDOLEUK MEDCEPEMENT
N; Alternate names: calpain chain L-1; calpain I catalytic chain; low-calcium requiring, N; Contains: chemotactic factor	306 REPLOBEDE THUCK DUTTERCHIOCI VEDDII CUMDAI DAMMACAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA
C; Species: Homo sapiens (man) C; Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text channe 08-Dec-2000	230 DESCRIPTION DE L'ACTUAL DE
213; A36740; S10591 oh: S · Ohno S · Emort V · Wolfe M · Woonky C · Committee	555 AUFRICE INDIFICATION TO THE TOTAL TO THE TOTAL TOT
NOIKE, M.; MOSAKI, G.; SUZUKI, K.	
A; Title: Complete amino acid sequence of the large subunit of the low-Ca2+-requiring for A; Reference number: A26213; WOID:86301172	KIRLDETODPODYGDRESGCSFVLA
A;Accession: A26213 A;Molecule type: mRNA	Qy 410 ASIPGKHYQAVGLHLWKYEKRKNIDENY-LSMPPVAGTACHAYDREVHLRCELS 462
A;Residues: 1-714 <aok> A;Cross-references: EMBL:X04366: NTD:029663: DTDN:02827881 1: DTD:020664</aok>	Db 435GRDMETIGFAVYEVPPELVGQPAVHLKRDFFLANASRARSEQFINLREVSTRFRLP 490
R; Kunimatsu, M.; Higashiyama, S.; Sato, K.; Ohtubo, I.; Sasaki, M.	KDAP
A;Title: Calcium dependent cysteine proteinase is a precursor of a chemotactic factor fo	
A; Kelerence number: A36740; MUID:90056492 A; Accession: A36740	
A;Molecule type: protein A;Residues: 2-10 <kun></kun>	RESULT 3
A; Experimental source: erythrocytes R; Sorimachi, H.; Ohni, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Minami, Y.; S	calpain (EC 3.4.22.17) large chain 3 - human N'Alternate names: calpain chain 1-3: calpain III catalutic chain: muscle specific
, 1990 ent cysteine protesse family	C.Species: Homo sapiens (man)
A:Reference number: S10589; MUID:90380278	C.Accession: A56218; A34488
Note: comparison with other gene products Comment: Calpain With other pene products	K;Kichard, 1.; Broux, O.; Allamand, V.; Fougerousse, F.; Chiannilkulchai, N.; Bourg, J.A.; Fardeau, M.; Jackson, C.E.; Cohen, D.; Beckmann, J.S.
C;Genetics: Carpain	Cell 81, 27-40, 1995 A:Title: Mutations in the proteolytic enzyme calpain 3 cause limb-girdle muscular dy:
	A; Reference number: A56218; MUID:95236448 A; Accession: A56218
A: Map position: lipter-ligter C:Complex: heterodimer of L (large) and S (small) chains	A;Status: not compared with conceptual translation A;Molecule type: mRNA
C;Function: A;Description: catalyzes the hydolysis of peptides	A;Residues: 1-821 <ric> A:Cross-references: GB:X85030: NID-c791039: PIDN-CAA59403 1: PID-c791040</ric>
A; Note: cleaves preferentially after tyrosine, methionine, or arginine residues and before; Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain	R:Sorimachi, H.; Imajoh-Ohmi, S.; Emori, Y.; Kawasaki, H.; Ohno, S.; Minami, Y.; Suzı J. Biol, Chem. 264, 20106-20111, 1989
C:Keywords: acetylated amino end; calcium binding; cysteine proteinase; duplication; EF F: 2-714/Product: calpain large chain 1 *status predicted <mat></mat>	A; Title: Molecular cloning of a novel mammalian calcium-dependent protease distinct i A; Reference number: A94688; MUID:90062125
F:85-33/Domain: calpain catalytic domain homology <calp> F:40-47/Domain: calpain catalytic domain homology <calp> F:40-57/Armsin: calpain catalytic domain homology <calp></calp></calp></calp>	A;Accession: A34488 A;Molecule type: mRNA
F;585-617/Domain: calmodulin repeat homology <ef1></ef1>	A;Residues: 44-445,'AA',448-458,'P',460-461,'P',463-484,'T',486-821 <sor> C;Genetics:</sor>

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C;Superiamiz;
C;Reywords: calcium binding; C;C;Reywords: calcium binding; C;Feyezords: calcium binding; C;Feyezords: calcium calcin catalytic domain.
F;649-680/Domain: calmodulin repeat homology <EF1>F;649-724/Domain: calmodulin repeat homology <EF2>F;725-724/Domain: calmodulin repeat homology <EF2>F;725-734/Domain: calmodulin repeat homology <EF3>F;757-789/Domain: calmodulin repeat homology <EF5>F;790-821/Domain: calmodulin repeat homology <EF5>F;129,334,358/Active site: Cys, His, Asn #status pred
RESULT 4

$38361

Calpain (EC 3.4.22.17) II large chain - rat

N;Alternate names: calpain II 80K chain

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change

C;Accession: $38361; $08650; $39751

R;DeLuca, C.I.; Davies, P.L.; Samis, J.A.; Elce, J.S.
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A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and befc
C;Superfamily; calpain large chain; calmodulin repeat homology; calpain catalytic domain
C;Reywords: calcium binding; cysteine proteinase; EF hand; hydrolase; muscular dystrophy
F;99-267,323-400/Domain: calpain catalytic domain homology #status atypical <CALP>
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A;Cross-references: GDB:119751; OMIM:11-
A;Map position: 15pter-15qter
A;Note: defects in this gene can cause
C;Complex: heterodimer of L (large) and
C;Function:
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Best Local Similarity
Matches 178; Conserv
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                                                                                                                                                                                                                                                                MHGNKQHLQKDFFLYNASKARSKTYINMREVSQRFRLPPSEYVIVPSTYEPHQEGEFILR
                                                                                                                                                                                                                                                                                               ---EKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGEFLLR 484
                                                                                                                                                                                                                                                                                                                                                                SEV----YIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAVGLHLWKV---
                                                                                                                                                                                                                                                                                                                                                                                                  ----LQSDKLQTWTVSVNEGRWVRGCSAGGCRN---FPDTFWTNPQYRLKLLEEDDDPDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYVDPEFPPDETSLFYSQKFPI-QF----VWKRPPEICENPRFIIDGANRTDICQGELGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CWFLAAIACLTLNOHLLFRVIPHDQS--FIENYAGIFHFQFWRYGEWVDVVIDDCLPTYN
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Pred. No. 1.9e-40;
9; Mismatches 194;
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                                                                    22-Jun-1999
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C:Superfamily: calpain large chain; calmodulin repeat homology; C:Keywords: calcium binding; cysteine proteinase; duplication; I F;75-327/Domain: calpain catalytic domain homology <EF1>F;529-560/Domain: calmodulin repeat homology <EF1>F;572-604/Domain: calmodulin repeat homology <EF2>F;607-604/Domain: calmodulin repeat homology <EF3>F;637-669/Domain: calmodulin repeat homology <EF3>F;637-669/Domain: calmodulin repeat homology <EF3>F;637-669/Domain: calmodulin repeat homology <EF3>F;105,262,286/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L09120; NID:g402665; PIDN:RAA16327.1; R;Samis, J.A.; Back, D.W.; Graham, E.J.; Elice, J.S. submitted to the EMBL Data Library, February 1990
A;Reference number: S08650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-700 < DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X51772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 380-439 <SAM>
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LPPGEYVLVPSTFEPHKNGDFCIRVFSEKKADYQTV
                                     LSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI
                                                                                                                                                                                                       N-NSGFPSNPKFWLRVSEPSE---
                                                                                                                                                                                                                                                   MSFSDFLRHYSRL
                                                                                                                                                                                                                                                                                   VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHT----RALPGAWVKGQSAGGCR
                                                                                                                                                                                                                                                                                                                           TGAEEVE-SSGSLQKLIRIRNPWGQVEWTGKWNDNCPSWNTVDPEVRANLTERQEDGEFW
                                                                                                                                                                                                                                                                                                                                                SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW : |:-|| | : | | : ::|||||
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                                                                               IGFGIYEVPEELTGQTNIHLSKNFFLTTRARERSDTFINL-
                                                                                                                                                           NYPNTFWMNPQYLIKLEEEDEDDEDGERGCTFLVGLIQKHR-----RRQRKMGEDMHT
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                                                                                                                   -SWSPASIPGKHYQAVGLHLWK----VEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCE
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                                                                                                                                                                                                                                           -EICNLTPDTLTCDSYKKWKLTKMDGNWRRGSTAGGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                             REVLNRFK
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EF hand;
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calpain (EC 3.4.22.17) large chain 2, tissue-specific C; Species: Rattus norvegicus (Norway rat) C; Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #te C; Accession: A48764; B48764 R; Sorimachi, H.; Ishiura, S.; Suzuki, K. J. Biol. Chem. 268, 19476-19482, 1993 A; Title: A novel tissue-specific calpain species expre
                                                                                                                                                   #text_change
                                                                                                                                                   20-Jun-2000
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expressed

predominantly in

us-09-768-877-2.sep19.rpr

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Absorribution: catalyzes the hydolysis of peptides
A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and
C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic dor
C;Superfamily: calpain large chain; calmodulin repeat homology; cysteine proteinase; EF hand; het.
E;2-700/Product: calpain large chain 2 *status predicted <AMT>
E;72-37/Domain: calpain catalytic domain homology <CALP>
E;52-700/Domain: calmodulin repeat homology <EF1>
E;52-560/Domain: calmodulin repeat homology <EF2>
E;603-664/Domain: calmodulin repeat homology <EF3>
E;603-669/Domain: calmodulin repeat homology <EF4>
E;637-669/Domain: calmodulin repeat homology <EF4>
E;27-604/Domain: calmodulin repeat homology <EF4>
E;27-669/Domain: calmodulin repeat homology <EF4>
E;2
                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-700 <SOR>
A;Residues: 1-700 <SOR>
R;Imajoh, S.; Aoki, K.; Ohno, S.; Emori, Y.; Kawasaki, H.; Sugihara, H.; Suzuki, K.
Biochemistry 27, 8122-8128, 1988
A;Title: Molecular cloning of the cDNA for the large subunit of the high-Ca(2+)-requ
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA; protein
A; Residues: 1-210, 1', 212-394, 'D', 396-445, 'I', 447-700 < LMA>
A; Residues: 1-210, 1', 212-394, 'D', 396-445, 'I', 447-700 < LMA>
A; Cross-references: GB:M2354; IDD:9511636; PIDN:AAA35645.1; PID:9511637
A; Cross-references: GB:M2354; ID:9511636; PIDN:AAA35645.1; PID:9511637
B; Mate, A.; Ohno, S.; Akita, Y.; Suzuki, K.
J. Biol. Chem. 264, 6404-6411, 1989
A; Title: Tandemly reiterated negative enhancer-like elements regulate transcription
A; Reference number: A33529; MUID:89197947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-67,'G','G','IE',75-78,'R' <HAT>
Cross-references: DDBJ:J04700; NID:g179910; PIDN:AAA52760.1; PID:g463086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356
         Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990
A;Title: A novel member of the calcium-dependent cysteine protease family.
A;Reference number: S10589; MUID:90380278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 PCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VYIAVLORSRLHAADWAGRARALVGDSHT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 PTKDGELEVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGLAEWYELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAEEVESN-GSLOKLIRIRNPWGEVEWTGRWNDNCPSWNTIDPEERERLTRRHEDGEFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHT-----RALPGAWVKGQSAGGCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       idene: GDB:CAPN2; mCANP; CANPm1

;Cross-references: GDB:119750; OMIM:114230

;Map position: 1pter-lqter

;Complex: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 608; DB 1; L
Pred. No. 9.7e-40;
74; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.7%;
Best Local Similarity 30.8%;
Matches 159; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-NSGFPSNPKFWLRVSEPSE-
                                                                                                                                                                                                                                                                                                                                  Accession: A31218
                                                                                                            Accession: S10590
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                                                                                  A; Molecule type: DNA; protein
A; Residues: 1-703 <SOR>
A; Cross-references: GB:D14479; NID:g441199; PIDN:BAA03370.1; PID:g441200
A; Resperimental source: stomach
A; Mote: sequence extracted from NCBI backbone (NCBIN:137770, NCBIP:137771)
A; Accession: B48764
A; Status: preliminary
A; Molecule type: DNA; protein
A; Residues: 1-379, SS2, SS0.2>
A; Cross-references: GB:D14480; NID:g441201; PIDN:BAA03371.1; PID:g495223
A; Cross-references: GB:D14480; NID:g441201; PIDN:BAA03371.1; PID:g495223
A; Cross-references: GB:D14480; NID:g441201; PIDN:BAA03371.1; PID:g495223
A; Cross-references: calpain large chain; calmodulin repeat homology cALP>
C; Keywords: alternative splicing; cysteine proteinase; EF hand; hydrolase
E; 732-563/Domain: calpain repeat homology <EPI>
F; 755-563/Domain: calmodulin repeat homology <EPI>
F; 512-563/Domain: calmodulin repeat homology <EPI>
F; 512-562,286/Active site: Cys, His, Asn #status predicted
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N;Alternate names: calpain chain L-2; calpain II catalytic chain; high-calcium
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999
C;Accession: S10590; A31218; A33529
R;Sorimachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:| || || |:| :|| || |:
L.K.DPEFPACPSALGYRDLG-PGSPDTGGIVWRRPTELCPNPQFIVGGATRIDIRQGGLG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPGKHYQAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCV-LSPRAGA-----RELGEFHAFIVSDL 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VYIAVLQRSRLHAADWAGRARALVGDSHTS--WSPA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 612; DB 2; Length 70
31.2%; Pred. No. 4.7e-40;
tive 87; Mismatches 197; Indels
number: A48764; MUID:93374936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 31.2
                                                           Status: preliminary
Molecule type: DNA; protein
Residues: 1-703 <SOR>
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Best Local Simi
Matches 155; (
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C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain C;Keywords: calpain catalytic domain cysteine proteinase; EF hand; hydrolase F;99-400/Domain: calpain catalytic domain homology #status atypical <CALP>
F;649-680/Domain: calmodulin repeat homology <EF1>
F;692-724/Domain: calmodulin repeat homology <EF3>
F;752-754/Domain: calmodulin repeat homology <EF3>
F;757-789/Domain: calmodulin repeat homology <EF3>
F;757-789/Domain: calmodulin repeat homology <EF4>
F;790-821/Domain: calmodulin repeat homology <EF5>
F;129,334,358/Active site: Cys, His, Asn #status predicted
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B34488
Calpain (EC 3.4.22.17) large chain 3 - rat
N;Alternate names: cysteine proteinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10 Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B34488; S10589
R;Sorimachi, H.; Imajoh-Ohmi, S.; Emori, Y.; Kawasaki, H.; Ohno, S.; Minami,
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A. Fitle: Molecular clothing of a novel mammalian calcium-dependent protease A; Reference number: A94688; MUID:90062125
A. Molecular clothing of a novel mammalian calcium-dependent protease A; Recession: B34488
A. Molecular clothing of a novel mammalian calcium-dependent protease A; Accession: B34488
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A;Title: A novel member of the calcium-dependent cysteine protease family.
A;Reference number: S10589; MUID:90380278
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Best Local Similarity 31.0
Matches 170; Conservative
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                                                                              PWGRRCWOGIMREGGEGWSQVDAAVASELLSQL-QEGEFWVEEEEFIREFDELTVGYPVT
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                                                                                                                                                                                                                                                                                                                                                                                      NQLVFTKSNHRNEFWSALLEKAYAKLHGSYEALKGGNTTEAMEDFTGGVTEFFEIKDAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.4%; Score 599.5; DB 1 31.0%; Pred. No. 5.6e-39; tive 78; Mismatches 186
                                                                                                                                                                                                                                                                                                                                 -----GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLI
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N;Alternate names: m-calpain heavy chain

C;Species: Gallus gallus (chicken)

C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000

C;Accession: S57194

R;Sorimachi, H; Tsukahara, T; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzuki,

Biochim. Biophys. Acta 1261, 381-393, 1995

A;Title: Identification of a third ubiquitous calpain species - chicken muscle & A;Reference number: S57194; MOID:95260862
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A; Residues: 1-700 < SOR>
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A:Accession: S57194
A:Status: preliminary
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                                                       TRRHEDGEFWMAFNDFLRHYSRLEICNLTPDTLASDRYKKWS--LL-
     SAGGCRN-NSGFPSNPKFWLRVSEPSE--
                                                                                                                                                             KLVKGHAYSVTGAEEVNFR-GSIQKLIRIRNPWGEVEWTGKWNDNCPNWSGVDPEVRERL
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Pred. No. 6.5e-39;
1); Mismatches 203
-VYIAVLQRSKLHAADWAGRARAL
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STO TAGGCRNYPNTEWINPOYLIKLEEEDEDPDDPEGGCTFLIGLIGKHRRKORKM 422	QY 472 TELKDAPGEFLLRVFSTGRVSLS 494
OY 400 VGDSHT-SWSPASIPGKHYQAVGLHLMKVEKRRVNLPRVLSMPPVAGTACHAYDRE 454	:
Oy 455 VHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI 496	RESULT 10 A55054 calpain (EC 3.4.22.17) large chain - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Dafte: 08-111-1995 #sequence revision 03-bun-1995 #foot chance 10-1000
RESULT 9 S57196 Calpain (EC 3.4.22.17) large chain 3 - chicken N'Alternate names: calpain p94 heavy chain; n-calpain-1 heavy chain C.Species: Gallus gallus chicken	ises rear_change
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C; Accession: S57196 C; Accession: S57196 F; Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishlura, S.; Suzuki, K. Biochim. Biophys. Acta 1261, 381-393, 1995 A; Title: Identification of a third ubiquitous calpain species - chicken muscle expresses	A; Accession: Aboust A; Accession: Aboust A; Status: preliminary: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-805 < EMO> A; Cross-references: GB:X78555; NID: 9562287; PIDN: CAA55297.1; PID: 9562288 C: Genetics:
	A;Gene: FlyBase:CalpA A;Cross-references: FlyBase:FBqn0012051 C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic do: C;Keywords: cysteine proteinase; duplication; EF hand; hydrolase F;90-347/Domain: calpain catalytic domain homology <calp></calp>
	F;0/0-/U8/JOMMAIN: Calmodulin repeat homology <ef1> F;7/09-738/Domain: calmodulin repeat homology <ef2> F;7/41-773/Domain: calmodulin repeat homology <ef3> F;7/4-805/Domain: calmodulin repeat homology <ef4></ef4></ef3></ef2></ef1>
Query Match 16.2%; Score 589.5; DB 1; Length 810; Best Local Similarity 28.6%; Pred. No. 3.3e-38; Matches 161; Conservative 87; Mismatches 178; Indels 137; Gaps 19:	Query Match 16.1%; Score 588; DB 1; Length 805; Best Local Similarity 30.0%; Pred. No. 4.4e-38; Matches 162; Conservative 84; Mismatches 200; Indels 94; Gaps 18;
PDDPREGOVKOGLLGD 72 :	OY 13 LFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDFREGOVKQG 68
OY 73 CWFLCACAALQKSRHLLDQVIPPGQPSWADQBYRGSFTCKIWOFGRWVEVTTDDRLPCLA 132	Qy 69 LLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWOFGRWVEVTTDDRL 128                   : :
QY 133 GRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188 1	QY 129 PCLAGRLCFSRCQREDVFWLPLLEKYYAKVHGSYBHLWAGQVADALVDLTGGLAERWNLK 188
	QY 189 GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGAR 232
GQODRPGRWEHRTCROLLHLKDQCLISCCVLSPRAGARELGEFHAFIVSDLRELQGQAGQ   :	OY 233 ELGEFHAFIVSDLRELQGQAGQCILLLRIQNPWGRRC-WQGLWREGGEGWSQVDAAVASE 291
	QY 292 L-LSQLQEGEFWVEREFFRELREYGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQ 350 : 1: 1   : ::    : ::         DD 334 IGLTPDRDGEFWMSFQDFLNHFDRYEICNLSPDSLTEDQQHSGKRKWFMSMYEGEWTPGV 393
Qy 314 ELTVGYPVTEAGHLQSLYTERLLCHTRAL-PGAWVRGQSAGGCRN-NSGFPSNPKFWLRV 371 :  :	QY 351 SAGGCRN-NSGFPSNPKFWLRVSEPSEVIAVLQRSRLHAADWAGRARALVG 401 ::
	OY 402 DSHTSWSPASIPGKHYQAVGLHLWKVEKRRY-NLPRVLSMPPVAGTACHAYD-REVH 456  1 :
	Qy 457 LRCELSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAIRAVAKNTTPGAALP 510   1   1   1   1   1   1   1   1   1   1

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C:Accession: JC5772
R:Mugita, N.; Kimura, Y.; Ogawa, M.; Saya, H.; Nakao, M.
Biochem. Biophys. Res. Commun. 239, 845-850, 1997
A:Title: Identification of a novel, tissue-specific calpain
A;Reference number: JC5772; MUID:98042481
                                                                                          tissue-specific calpain htra-3 - human
C;Species: Homo sapiens (man)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1993
A;Description: Sequence of the C. elegans cosmid C06G4.
A;Reference number: S44747
A;Accession: S44749
A;Status: preliminary
A;Molecule type: DNA
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$44749
C0664.2 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: $44749
R;Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-653 <WAT>
                                                                                                                                                                                                                                                                                                                 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMGLKFDHDGEFWMSFDDFMRNFEKMEICNLGPDVMDEVYQMTGVKAAGMVWAANTHDGA
                                                                                                                                                                                                                                                                        ELSPGYYLAVPSTFLKDAPGEFLLRVFSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGDCWLLAAAANLTLKDELFYRVVPPDQS--FTENYAGIFHFQFWQYGKWVDVVIDDRLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLP 129
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Pred. No. 1.7e-37;
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C; Superfamily: human tissue-specific calpain htra-3; calpain C; 148/Domain: I #status predicted <IDD>
F; 1-48/Domain: I #status predicted <IDD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: htra-3
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A; Residues: 1-647 < MUG>
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A; Status: nucleic a
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLGD
                 13
                                                                 SVFLRTDQPEGRYVIIPTTFEPGHTGEFLLRVFT
                                                                                              EVHLRCELSPGYYLAVPSTFLKDAPGEFLLRVFS 487
                                                                                                                                     GKGENL
                                                                                                                                                GRARALVGDSHTSWSPASIPGKHYQAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDR |: | : | : : | :: : | :: : |
                                                                                                                                                                                               HGAWTLHEDPRQNRGGGCINHKDTGF-QNPQYIFEVKKPEDEVLICIQQRPKRSTRERRE
                                                                                                                                                                                                                                 PGAWY-----KGOSAGGCRN--NSGFPSNPKFWLRVSEP-SEVYIAVLQRSRLHAAD-WA
                                                                                                                                                                                                                                                                                                  VASELLSQLQ-EGEFWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCH----TRAL
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                                                                                                                                                                                                                                                                EREKMGVTVQDDGEFWMTGEDVCR----YEFTDIIKCRVINTSHLSIHKTWEEARL
                                                                                                                                                                                                                                                                                                                                   TTHAYAVTDVRKVRLTTHTLLAFFKSEKLDMIRLRNPWGEREWNGPWSDTSEEWQKVSKS
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                                                                                                                                  -----AIGFDIYKVEENROY--RMHSLQHKAASSIYINSR
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Pred. No. 9.4e-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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R;Barnes, T.M.; Hodgkin, J.
EMBO J. 15, 4477-4484, 1996
A;Title: The tra-3 sex determination gene of Caenorhabditis elegans encodes a A;Reference number: S71885; MUID:97042339
A;Accession: S71885

membe

A; Status: nucleic acid

sequence not shown

C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 29-Oct-1999

Caenorhabditis elegans

sex-determining protein transformer-3 - N;Alternate names: tra-3 protein C;Species: Caenorhabiltis elegans

C; Accession: S71885; T23631

```
A;Molecule type: mRNA
A;Residues: 1-14,'A',16-120,'A',121-127,'H',129-213,'R',215-384,'VTC',388-440,'S',44
A;Cross-references: GB:W14233; NID:g160934
A;Note: sequence extracted from NCBI backbone (NCBIP:79194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Molecular cloning and sequence analysis of a calcium-activated neutral prof
                                                                                                                                encoding a novel calcium-activated neutral
                                                                                                                                                                                                                                                                                                A;Residues: 1-758 <AND>
A;Cross-references: GB:M67499; NID:g160936; PIDN:AAA29858.1; PID:g160937
R;Karcz, S.R.; Podesta, R.B.; Siddiqui, A.A.; Dekaban, G.A.; Strejan, G.H.; Clarke, Mol. Biochem. Parasitol. 49, 333-336, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic C; Keywords: calcium binding; cysteine proteinase; duplication; EF hand; hydrolase F;124-380/Domain: calpain catalytic domain homology <CALP>
F;628-660/Domain: calmodulin repeat homology <EF1>
F;661-690/Domain: calmodulin repeat homology <EF2>
F;661-690/Domain: calmodulin repeat homology <EF2>
F;693-726/Domain: calmodulin repeat homology <EF2>
F;727-758/Domain: calmodulin repeat homology <EF4>
F;727-758/Domain: calmodulin repeat homology <EF4>
F;154,313,337/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NOKERPS------DLIDQLKIYAQRCCIMGCSIDSSVMEQKMDNGLIGS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - HAYSLIGVYPV-NYRGRIQMIAMRLRNPWGDSHEWKGAWCDGSPQWREISEQEKKNINLS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 LAG--RLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 FTADGEFWMSYEDFCYLFSRVEVCHLGLESLEYNQNFHGKRRL-DEAIFSGGWQRNVNAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 PGKHYQAVGLHLMKVE---KRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTLWEDPDFPANDKAI----GNLPDFRERIEWKRPLEINPNAKFFAGGASRFDIEQGAL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCINNRITYWINPQFRITVEDPD-------PDDDDNKCSVLIGLMQTDIRKK-- 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 VGADFQPIGFMVYNAPDDLNTLLSRAQLLTRSPIAKSQ-FINTREVTAQFRVPPGSYVVI 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVAGSGGQQDRPGRWEHRTCRQLLHLKDQ-----CLISC----CVLSPRAGARELGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 FHAFIVSDLRELQGQAGQCILLLRIQNPWG-RRCWQGLWREGGEGWSQVDAAVASEL-LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 QLQEGEFWYEEEFFLREFDELTYGYPYTEA-GHLQSLYTERLLCHTRALPGAWYKGQSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 GCRNN-SGFPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.8%; Score 540; DB 1; Length 75 Best Local Similarity 30.0%; Pred. No. 2.4e-34; Matches 155; Conservative 77; Mismatches 219; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSTFLKDAPGEFLLRVFSTGRVSLSAIRAVAKNTTPG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A45642; MUID:92131071
A; Accession: A45642
                                             R; Andresen, K.; Tom, T.D.; Strand, M.

Biol. Chem. 266, 15085-15090, 1991
A; fitle: Characterization of cDNA clones
A; Reference number: A39343; MUID:91332027
A; Accession: A39343
A; Accession: A39343
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description: required for the correct sexual development of soma and germ line in herm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: fully dispensable in males Superfamily: human tissue-specific calpain htra-3; calpain catalytic domain homology 53-336/Domain: calpain catalytic domain homology <CALP>
                                                                                                  R; Matthews, L.

Submitted to the EMBL Data Library, November 1996
A; Reference number: 219775
A; Reference number: 219775
A; Reference number: 219775
A; Accession: T23631
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-648 <WIL>
A; Residues: 1-648 <WIL>
A; Residues: 1-648 <WIL>
A; Gross-references: EMBL: 282277; PIDN: CAB05248.1; GSPDB: GN00022; CESP: LLC1.1
A; Experimental source: Clone LLC1
C; Genetics:
A; Gene: tra-3
A; Map position: IV; 4
A; Introns: 78/3; 142/3; 205/3; 273/3; 394/3; 513/3; 581/3
C; Function:
A; Description: required for the correct sexual development of soma and germ line
A; Note: fully dispensable in males
C; Superfamily: human tissue-specific calpain htman tissue-specific calpain homology <CALPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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C;Species: Schistosoma mansoni
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHVRKFL-----KDDPNDTELKLFNDLKTAFDKGALVVAAIAART-KEEIEESLDCGLVK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRLPCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAER 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDAAVASEL-----LSQLQEGEFWVEEEFFLREFDELTVGYPV-TEAGHLQSLYTERLLC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTRALPG -- AWVKGQSAGGCRN-NSGFPSNPKFWLRVSEPS-EVYIAVLQRSRLHAADWA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRARALVGDSHTSWSPASIPGKHYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAYD 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KQPFVDTLFPPTNQSLFLE-----QRQSSDIVWKRPGELHPDPHLFVEGASPNDVTQGIL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLL.70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -HAFIVS-----DLRELQGQAGQCIL-----LLRIQNPWGRRCWQGLWREGGEGWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEWITNGKKSGAPDDRAGGCHNFKATFCNNPQYIFDIPSPNCSVMFALIQNDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SEGLKKREPFVTIGMHVMKVENNRQY--RVHTAMHPIA-ISDYASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%; Score 569; DB 2; Length 648; 28.8%; Pred. No. 1e-36; Live 93; Mismatches 217; Indels 106;
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A;Residues: 1-648 <BAR>
A;Cross-references: EMBL:U12920
A;Experimental source: strain N2
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Best Local Similarity 28.8%
Matches 168; Conservative
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N;Alternate names: mu-calpain heavy chain
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S57195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: mRNA;

Residues: 1-586 <SOR>
;Residues: 1-586 <SOR>
;Cross-references: EMBL.D8027; NID:g882070; PID:g882071
;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain;
;Superfamily: cysteine proteinase; EF hand; hydrolase
;Reywords: cysteine proteinase; EF hand; homology (fragment) <CALP>
;1-208/Domain: calpain catalytic domain homology (fragment) <CALP>
;457-489/Domain: calmodulin repeat homology <EF1>
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Best Local Similarity
Matches 132; Conserv
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Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzuki, K. ochim. Blophys. Acta 1261, 381-393, 1995
Title: Identification of a third ubiquitous calpain species - chicken muscle expresses
Reference number: S57194; MUID:95260862
         380
                                                 480 EFLLRVFSTGR 490
                                                                                                        332
                                                                                                                                   424 LWK----VEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPG 479
                                                                                                                                                                                    279 GDDFGGREPGCSFLLALMQKHR-----RRERRYGKDMETIGFAVYEVPPEHVGRSGVH
                                                                                                                                                                                                                                                                                                                            322 TEAGHLOSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFPS----NPKFWLRVSEPSE- 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 LPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVAGSGGQQDRPGRWEHRT 207
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DFVLRVFSEKR 390
                                                                                                                                                                                                                                                                                PDA--LQSRKFRK--WNTRLYDGSWRRGSTAGGCRN---YPATFWINPQFKICLEEVDDD 278
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73; Mismatches 157;
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Sequence 10, Appl	٥ į	٠.	N	ω	Sequence 9, Appli	Α	94,	Sequence 94, Appl		96	•	99,	98,	•	Sequence 95, Appl	rddy 'ce anienbec	2	Sequence 97, Appl

## ALIGNMENTS

; LENGTH: 672 ; TYPE: PRT ; ORGANISM: Human US-09-422-869-2 US-09-422-869-2 SOFTWARE: PatentIn Ver. SEQ ID NO 2 APPLICANT: POLONSKY, KENNETH APPLICANT: HORIKAWA, YUKIO APPLICANT: ODA, NAOHISA APPLICANT: COX, NANCY J. APPLICANT: SREENAN, SEAMUS GENERAL INFORMATION: Sequence 2, Application US/09422869 Patent No. 6235481 CURRENT APPLICATION NUMBER: US/09/422,869 CURRENT FILING DATE: 1999-10-21 EARLIER APPLICATION NUMBER: 60/134,175 EARLIER FILING DATE: 1999-05-13 APPLICANT: ZHOU, YUN-FING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAEME I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307 NUMBER OF SEQ ID NOS: 30 KENNETH S.

δÃ B Ş 밁 ş Вρ Query Match
Best Local Similarity 100.0%; 1
Matches 672; Conservative 0; 181 61 REGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 61 REGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 120 LAERWNLKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF LAERWNLKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF Score 3649; Pred. No. 0; O; Mismatches 0; Indels 0 Gaps 240 240 120

DB 4;

Length 672;

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241 IVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGE 300

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FWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG 360
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APPLICANT: HORINAM, YUKIO
APPLICANT: HORINAM, YUKIO
APPLICANT: COX, NAOHISA
APPLICANT: COX, NAOHISA
APPLICANT: COX, NAOHISA
APPLICANT: SREENAN, SEAMUS
APPLICANT: STRENAN, SEAMUS
APPLICANT: HOWING
APPLICANTON: NUMBER: 05/09/422,869
CURRENT APPLICATION NUMBER: 60/134,175
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER APPLICATION NUMBER: 60/134,175
SOFTWARE SEQ ID NOS: 30
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81.1%; Pred. No. 3.7e-289;
ive 45; Mismatches 76;
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APPLICANT: POLONSKY, KENNETH S.
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: DOBA, NANCHSA
APPLICANT: COBA, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: STEENAN, SEBANGS
APPLICANT: CTANI, KENICHI
APPLICANT: CTANI, KENICHI
APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, RENICHI
APPLICANT: OTANI, RENICHI
APPLICANT: OTANI, RENICHI
CORRENT: BELL, GRAEME I.
FILE REFERENCE: ARCD:30
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER PILING DATE: 1999-10-21
SEQLIER PELICATION NUMBER: CO/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 18
LENGTH: 666
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Patent No. 6235481
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; LENGTH: 544 ; TYPE: PRT ; ORGANISM: Human US-09-422-869-4

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                 CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                  APPLICANT: POLONSKY, KEN
APPLICANT: HORIKAWA, YUK
APPLICANT: ODA, NAOHISA
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                  APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF
FILE REFERENCE: ARCD: 307
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COX, NANCY J.
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FLLRVFSTGRVSLRALAPAASASLCISTAGPVTPSSTPSASI 522
                                           GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE
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Pred. No. 5.5e-263;
                     -NTTPGAAL 509
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SOFTWARE: PatentIn V
SEQ ID NO 8
LENGTH: 513
TYPE: PRT
ORGANISM: Human
                                                                                                CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09422869 Patent No. 6235481
                                                                                                                                                                                                                 APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF
                                                                                                                                                                                                      FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                          APPLICANT: ODA, NAOHISA APPLICANT: COX, NANCY J.
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us-09-768-877-2.sep19.rai

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Gaps

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Length 444; Indels

Score 2336; DB 4; Pred. No. 2.3e-226; 1; Mismatches 0;

64.0%;

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Similarity

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Matches 425;
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APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: STEAMUS
APPLICANT: STEAMUS
APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, KENICHI
APPLICANT: HIS, CRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REPERENCE: ARCD:307
CURRENT FILING DATE: 1999-10-21
EANLIER APPLICATION NUMBER: 60/134,175
SARLIER FILING DATE: 1999-10-21
SARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                       Length 513;
                                                              Indels
                                     Score 2699; DB 4;
Pred. No. 8.9e-263;
1; Mismatches 8;
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Patent No. 6235481
                                   Query Match
Best Local Similarity 98.2%;
Matches 496; Conservative
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; ORGANISM: Human
US-09-422-869-10
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US-09-422-869-8
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LENGTH: 444
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TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2
FILE REFERENCE: ARCD:307

CURRENT APPLICATION NUMBER: US/09/422,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 858.5; DB 4
Pred. No. 4.6e-78;
1; Mismatches 13
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EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09422869
Patent No. 6235481
GENERAL INFORMATION:
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APPLICANT: COX, NANCY J.
APPLICANT: SREBNAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: OTANI, KENICHI
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Best Local Similarity
Matches 165; Conserv
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| 421 GLHLWK 426
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US-09-422-869-12
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US-08-835-099A-1
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                     TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                       NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-AP
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DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                            LFKDPEFPACPSALGYKDLG-PGSPQTQGIIWKRPTELCPSPQFIVGGATRTDICQGGLG 103
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    Application US/08835099A
    5874277

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                                                                                             Conservative
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KAWAMOTO, Tomo
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03-APR-1997
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                                                                                        Score 635; DB 2; 1
Pred. No. 6.5e-55;
5; Mismatches 179;
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                                                                                                                     Length 703;
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US-09-157-349-1
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                                                                  APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: RESOLCK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02109
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            TELEPHONE: 01/ -523-6440
                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHINTANI, Yasushi
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                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                         DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                    Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOVEL PROTEINS, THEIR PRODUCTION
                                                                                                                                                                              08/835,099
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RWRKRIGOGMLS

430

378

325 302 242 218

INFORMATION FOR SEQ ID NO:

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CURRENT APPLICATION DATA
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                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 VEBEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFP 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                192 GSGGQQDRPGRWEHRTCRQLLHLKDQC---LISCCV-LSPRAGA-----RELGEFHAFIV
                                                                                                                                                                    Length 703;
                                                                                                                                                                                                     Indels
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APPLICANT: SHRYANI, Yasushi
APPLICANT: NISHI, Kaznoshi
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 WALER SLICEL
                                                                                                                                                                                                 85; Mismatches 179;
                                                                                                                                                              17.4%; Score 635; DB 3; 32.3%; Pred. No. 6.5e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 ELSPGYYLAVPSTFLKDAPGEFLLRVFS 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08835099A
Patent No. 5874277
                LENGTH: 703 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLEGULE TYPE: protein
US-09-157-349-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                           Best Local Similarity 32.39
Matches 164; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
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SOFTWARE: FastSE
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    US/08/835,099A
                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 085649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATONNEY/AGENI INFORMATION:
NAME: RESILCK, David S
REGISTRATION NUMBER: 34,235
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Patent No. 6068990
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.48;
                        04-APR-1997
V: 514
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Best Local Similarity 32.3%
Matches 164; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-835-099A-2
APPLICATION NUMBER:
FILING DATE: 04-AF
CLASSIFICATION: 51
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acid
 335 MSLSDFVRQFSRLEICNLSPDSLSSEEVHKWNLVLFN---
                            303 VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFP
                                                            276 TGVEEVNFQ-GHPEKLIRLRNPWGEVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFW
                                                                                           243 SDLREIQGOAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW
                                                                                                                           228 ------KPPANLYQIIRKAL-----CAGSLLGCSIDVSSAAEAEAITSQKLVKSHAYSV
                                                                                                                                                                                          171 NGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTVEGFEDFTGGISEFYDLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                       113
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
                                                                                                                                                                                                                                                                                   72 DCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCL 131
                                                                                                                                                                                                                                                                                                                        54 LFKDPEFPACPSALGYKDLG-PGSPQTQGIIWKRPTELCPSPQFIVGGATRTDICQGGLG 112
                                                                                                                                                                                                                                                                                                                                            13 LFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                        DCWLLAAIASLTLNEELLYRVVPRDQD--FQENYAGIFHFQFWQYGEWVEVVIDDRLPTK 170
                                                                                                                                                           GSGGQQDRPGRWEHRTCRQLLHLKDQC---LISCCV-LSPRAGA-----RELGEFHAFIV
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Pred. No. 6.6e-55;
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 -GHWTRGSTAGGCQN---YP
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; ORGANISM: Human
US-09-422-869-22
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                                                     SEQ ID NO 22
LENGTH: 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                          SOFTWARE: PatentIn
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
                                                                                                                                                                                                                                                    APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: HELY CONNIG L.
                                                                                                           EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                          EARLIER APPLICATION NUMBER: 60/134,175
                                                                                                                                                                                                  APPLICANT: BELL, GRAEME I.

TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
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                                      TYPE: PRT
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6235481
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  132 AGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGVA 191
                                      364 -- NPKFWLRVSEPSE--
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WVNPQFKIRLDETDDPDDYGDRESGCSFVLALMQKHR--
                                                              RDFMREFTRLEICNLTPDA--LKSRTIRK--WNTTLYEGTWRRGSTAGGCRN---YPATF
                                                                                              EEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSGFPS--
                                                                                                                                 KQV-NYRGQVVSLIRMRNPWGEVEWTGAWSDSSSEWNNVDPYERDQLRVKMEDGEFWMSF
                                                                                                                                                                                                              SDLYQ---
                                                                                                                                                                                                                                 GSGGQQDRPGRWEHRTCRQLLHLKDQCLISC----CVLSPRA-GARELGEFHAFIVSDL 245
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                               -VYIAVLQRSRLHAADWAGRARALVGDSHTSWSP
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--- GASLFTIGFAIYEVPKE 512
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329 SDFLKQYSRLEICNLSPDSLSSEEIHKWNLVLFN----GRWTRGSTAGGCLNYPGTYWTN 384
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                                   ---EKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGEFLLR
                                                           58;
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
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31.2%; Pred. No. 1.3e-52;
.ive 87; Mismatches 197;
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CURRENT PAPLICATION NUMBER: 05/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
BARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VAT. 2.0
                                                                                                                                            573 VFSEKRNLSEEVENTISVDRPVKKKKT 599
                                                                                                          485 VFSTGR-----VSLSAIRAVAKNTT 504
                                                                                                                                                                                                                                  Sequence 27, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                                                                                        APPLICANT: POLONSKY, KENNETH
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
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Best Local Similarity 31.2%
Matches 155; Conservative
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474 SEVICSFLVALMORNR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: RAT
US-09-422-869-27
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                                       435 ----GRDMETIGFAVYEVPPELVGQPAVHLKRDFFLANASRARSEQFINLREVSTRFRLP 490
                ---REVHLRCELS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CWFLCACAALQKSRHLIDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPCLA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ERWNLKGVA------GSGGQQDRPGRWEHRTCRQLLHLKDQCLISCC 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 DLDPRGSDERPTRIIPVQYETRMACGLVRGHAYSVTGLDEVPFK-GEKVKLVRLRNPWG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRCWQGLWREGGEGWSQVDAAVASELLSQL-QEGEFWVEEEEFLREFDELTVGYPVTEAG 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLLGD 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 GRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 VLSPRAG------ARELGEFHAFIVSDLRELGGAGQCILLLRIQNPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLOSLYTERLICHTRAL-PGAWVKGQSAGGCRNNSGFP----SNPKFWLRVSE-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEV----YIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPCKHYQAVGLHLWKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%; Score 618; DB 4; Length 821;
31.4%; Pred. No. 4.3e-53;
ive 79; Mismatches 194; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BELL, GRAEME I.

TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE REFERENCE: ARCD: 307
CURRENT PAPLICATION NUMBER: US/09/422,869
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALLING VET: 2.0
SEQ ID NO 24
LENGTH: 821
       410 ASIPGKHYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAYD--
                                                                            16.9%; Score 618;
                                                                                                                                                                                                          Sequence 24, Application US/09422869
Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.4%
Matches 178; Conservative
                                                                                                                                                                                                                                                                               HORIKAWA, YUKIO
ODA, NAOHISA
COX, NANCY J.
                                                                                                                                                                                                                                                                                                                                  APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-09-422-869-24
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TOPOLOGY: lin

MOLECULE TYPE:

HYPOTHETICAL: N
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                                                                                                                                                                                                                                                      Query Match 16.6
Best Local Similarity 30.4
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,525
FILING DATE: 07-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/487,942
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BFOWD, SCOET A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5258
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 876-585
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BENERAL INFORMATION:
APPLICANT: Lin, L
APPLICANT: Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equence 7, Application US/08726525 atent No. 5789181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
189 GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEF-----HAFIV 242
                                   159 PTKDGELLFYHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELK 218
                                                                129 PCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK 188
                                                                                                     101 ALGDCWLLAAIASLTLNEEILARVVPLNQS--FQENYAGIFHFQFWQYGEWVEVVVDDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Graham, James
TITLE OF INVENTION: NOVE
TITLE OF INVENTION: INTR-
                                                                                                                                                                                                  UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 STFLKDAPGEFLLRVFS 487
                                                                                                                                         69 LIGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRL 128
                                                                                                                                                                            42 AGTLFQDPSFPAIPSALGFKELG-PYSSKTRGMRWKRPTEICADPQFIIGGATRTDICQG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 STFEPFKDGDFCLRVFS 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                   : protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in, Lih-Ling
                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           876-5851
                                                                                                                                                                                                                                                  16.6%; Score 604; DB 1; Length 700; 30.4%; Pred. No. 8.4e-52; ative 76; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVEL INTERLEUKIN-1 RECEPTOR
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/726,525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI5258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DFFLGROPSTCSSTYMNLREVSSRVRLPPGQYLVVP 488
                                                                                                                                                                                                                                                    Indels 74;
                                                                                                                                                                                                                                                  Gaps
                                                                                                         158
                                                                                                                                                                                                                                                  15;
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Qy	Qy Db	Qy Db	Оy	Оy	Db .
461 477	406 429	357 376	303 326	243 267	219
461 LSPGYYLAVPSTFLKDAPGEFLLRVFSTGRVSLSAI 496 	406 -SWSPASIPGKHYQAVGLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCE 460 : : : : :	357 N-NSGFPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHT 405	303 VEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAMVKGQSAGGCR 356 : :	243 SDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFW 302 :  ::    :  :	: ::  :  :

Search completed: September 19, 2002, 14:49:17 Job time: 26 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                       Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                               2963
2719.5
2715.5
2701.5
2699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
            100.0
99.9
99.7
81.2
74.5
74.0
74.0
64.0
26.4
                                                                                                                                                                                                                                                                                                 Match
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747574 segs, 111073796 residues
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3649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRAGRGATPARELFRDAAFP.....SQEMLGQFLQEVSVMAVMKT 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990_DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991_DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994_DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997_DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.
                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
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       AAY79567
AAW70019
AAW93341
AAY79575
AAE09756
AAX79568
AAX79568
AAX79571
AAW25421
AAW79572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Search time 34.68 Seconds (without alignments) 2152.295 Million cell updates/sec
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Human calpain 10a.
Human protease and
Human polypeptide,
Wouse calpain 10.
Human calpain 10c.
Human calpain 10b.
Human calpain 10d.
Human calpain 10f.
                                                                                                                                                                                                                                                                                         Description
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	468	472	483.5	506	507	508.5	513.5	569	585	. 586	594.5	604	604	606	608.5	<b>610</b>	614	615.5	15.	615.5	615.5	618	635	635	636	641.5	641.5	644.5	644.5	644.5	644.5	644.5	644.5	644.5
	12.8	•	13.3			13.9	14.1	15.6	16.0	16.1	16.3	16.6	٠	• '	•	16.7	16.8	٠	16.9	16.9	16.9	16.9	17.4	17.4	17.4		17.6	17.7	17.7	17.7	17.7:	17.7	17.7	17.7
	1043	138	641	399	137	1069	139	791	565	828	640	700	700	133	757	700	700	640	640	513	513	821	712	703	144	787	787	739	723	702	702	702	702	686
	22	21	20	22	22	22	21	22	22	22	19	21	18	21	20	22	22	19	19	19	19	17	18	18	21	22	22	22	22	22	22	22	21	22
·	ABB60095	AAY79574	AAW93364	AAM41149 .	AAU23331	ABG26746	AAY79573	ABB63692	ABB66731	ABB63328	AAW63833	AAB37797	AAW19992	AAB41188	AAY30342	AAB86128	AAB86130	AAW63831	AAW59499	AAW63832	AAW59500	AAR99579	AAW41565	AAW41564	AAB41778	AAM80009	ABB12017	AAB62152	AAB62153	AAB46595	AAB62154	AAM79025	AAB40701	AAB62155
	で			_			Human calpain 10g	Drosophila melanog	Drosophila melanog	7	_		Human CANP used to	Human ORFX ORF952	A calpain protein	Human calpain 80kD	Rat calpain 80kDa				uncate	in large su	calpain.	_	Ξ.	protein	calpai	l human	•	testis		Human protein SEQ	ORFXO	Novel human protei

## ALIGNMENTS

RESULT AAY79567

15-AUG-2000 (first entry)

AAY79567;

AAY79567 standard; Protein; 672 AA

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WPI; 2000-339702/29.
N-PSDB; AAA27475, AAA27476.
                                   Polonsky KS, Horikawa Y, Oda N, Hanis CL, Bell GI;
                                                                         21-OCT-1998;
13-MAY-1999;
                                                         (ARCH-) ARCH DEV CORP.
                                                                                               21-OCT-1999;
                                                                                                               27-APR-2000.
                                                                                                                              WO200023603-A2
                                                                                                                                           Homo sapiens
                                                                                                                                                            therapy.
                                                                                                                                                                NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; calpain 10a; diapain-1; cysteine protease; diagnosis;
                                                                                                                                                                                         Human calpain 10a
                                                                         980S-0105052
990S-0134175
                                                                                               99WO-US24890
                                          Sreenan
                                          s
                                         Zhou Y,
                                          Otani K;
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Method for screening for type 2 diabetes mellitus comprises detecting a

us-09-768-877-2.sep19.rag

The present sequence is that of a novel human cysteine protease, designated calpain 10a. The protein is encoded by the major transcript (see AAAZ7476) of the human calpain 10 gene, CAPN10 (see AAZ7475), which has been identified in the NIDPM1 region of chromosome 2. The CAPN10 gene consists of 15 exons spanning 32 kb. chromosome 2. The CAPN10 gene consists of 15 exons spanning 32 kb. a complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see Invention concerns the identification of genes responsible for type 2 diabetes responsible for type 2 diabetes responsible for type 2 diabetes responsible for cype 2 diabetes responsible for shows evidence for linkage to type 2 diabetes. Claimed methods for snew softence for linkage to type 2 diabetes mellitus are based con detection of a polymorphism in a calpain encoding nucleic acid, especially ucsney of the CAPN10 gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding colympletide such as calpain activity using calpain 10 polypeptides: and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport.  $\operatorname{polymorphism}$  in a calpain encoding nucleic acid segment or protease-encoding nucleic acid segment -Claim 40; Page 217-219; 257pp; English. 

672 AA; Sequence

ö EVITIDDRIPCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSTEHLWAGQVADALVDLTGG 180 240 420 009 480 540 009 Gaps 9 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP LAERWNLKGVAGSGGOODRPGRWEHRTCROLLHLKDOCLISCCVLSPRAGARELGEFHAF FPSNPKFWLRVSEPSEVY I AVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV NPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDAPPLLLQEPL **PLLRVFSTGRVSLSAIRAVAKNTTPGAALPAGEWGTVQLRGSWRVGQTAGGSRNFASYPT GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE** ö DB 21; Length 672; Indels ; 100.0%; Score 3649; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 672; Conservative Query Match Best Local 3 61 61 121 121 181 241 181 241 301 301 361 361 121 481 181 421 541 ŝ g q ð 6 ò ð g ò g ò qq ŏ g ò q ò

99WO-US17818

06-AUG-1999;

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diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic; hepatototropic; antifilammatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic;
        LSCVPHRYAQEVSRLCLLPAGTYKVVPSTYLPDTEGAFTVTIATRIDRPSIHSQEMLGQF
                                                                                                                                                                                                                                                                                                                                                                              note= "Signature sequence of Cysteine protease"
                                                                                                                                                                                                              protein-13; PPRG-13; anti-PPRG antibody;
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Potential Phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Potential Phosphorylation site"
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13..322
/note= "Signature sequence of Calpain"
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                                                                                                                                                                                       Human Protease and associated protein-13 (PPRG-13).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O,
Corley NC,
                                                                                                                                                                  New human proteases, useful for diagnosis, treatment cell proliferative disorders such as atherosclerosis
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11-FEB-1999;
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                         FLLRVESTGRVSLSAIRAVAKNTTPGAALPAGEWGTVQLRGSWRVGQTAGGSRNFASYPT
                                                            2000-224346/19.
DB; AAZ50930.
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Yue H,
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99US-0119768
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YT, Reddy R,
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Pred. No. 0;
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R, Patterson C, Au-Young
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Matches Query Match Best Local

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Similarity

99.7%; 99.7%;

Score 3638; D Pred. No. 0; 0; Mismatches

DB 22;

Length Indels

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                clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                             The invention relates to primers for synthesising full
                                                                                                                                                                                             use
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Sequence
                                                                                                                                                                      Claim
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                                                                                                                                                                      8; SEQ
                                                                                                                                   830 cDNA molecules encoding a
                                                                                                                                                                                                                                                                           Nishikawa T,
                                                                                                                                                                  ID NO 2881; 1380pp + sequence listing; English.
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2000JP-0183765
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a T, Nagai
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K, Kojima
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REGOVKOGILGDCWF1CACAALOKSRH1LLDQV1PPGQPSWADQEYRGSFTCR1WQFGRWV
                                                                                                                                  GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE
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Calpain 10; diapain-1; mouse; diagnosis; therapy; NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene.
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       AAY79575 standard; Protein; 666
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99US-0134175,
                                   (first entry)
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                                                 Mouse calpain 10.
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                                                                                    Mus musculus
                                  15-AUG-2000
                                                                                                                            21-OCT-1999;
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                     AAY79575;
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The present sequence is that of murine calpain 10 (or diapain-1), a novel cysteine protease encoded by the major transcript of the CAPNIO gane (see AAAZ1484). Calpain is ubiquitously expressed in mouse and humans. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therefore (see AAAZ1475) shows evidence for linkage to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes are based on detection of a polymorphism in a calpain canciding nucleic acid. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polymuclectides. Calpain 10 polypeptides using calpain 10-encoding polymuclectides. Calpain 10 polypeptides using calpain 10 encoding cactivity using calpain 10 polypeptides will particular through the regulation of an insulin secretory response or insulin mediated
                                                                                                             is comprises detecting
segment or a
                                                                                                Method for screening for type 2 diabetes mellitus polymorphism in a calpain encoding nucleic acid se protease-encoding nucleic acid segment -
                                                                                                                                                                                      Claim 40; Page 234-236; 257pp; English.
                                     WPI; 2000-339702/29.
N-PSDB; AAA27484, AAY79574, AAY79576.
Bell GI;
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Hanis CL,
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240 EVITIDDRIPCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGG 180 300 300 360 FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV 420 GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE 480 FLLRVFSTGRVSLSAIRAVAKNTTPGAALPAGEWGTVQLRGSWRVGQTAGGSRNFASYPT 540 Gaps 9 9 61 REGOVROGILGDCWFICACAALORSRHILDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP FWVEEEEFLREFDELTVGYPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG LAERWNIKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHAF NPCFPFSVPEGPGPRCVRITLHQHCRPSDTEFHPIGFHIFQVPEGGRSQDAPPLLLQEPL 9 999 Length Indels ; Score 2963; DB 21; ; Pred. No. 2.1e-260; 45; Mismatches 76; 81.2%; 81.1%; Best Local Similarity 81.1 Matches 544; Conservative Query Match 121 121 181 241 241 301 301 361 421 **481** 475 541 g à ŏ g ò g ö g δ qq δ d ŏ ö g g ŏ a ŏ

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                                                                                                                                                                                                                                                                                                                                                                                   chromosome
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67.:78
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states that residues GATPAR
However residues GSFTCR are
                                                                                                                                                         given in the specification"
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                                    282..285
                                                                                                             189..194
                                                                                                                                                                                                                        cysteine active
                                                                                                                              123..126
                                                                                                                                                                                                                      /note= "Eukaryotic thiol (cysteine)
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13..322
                                                                                                                                        'note=
                                                                                                                                                                                                                                                                   'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                          note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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     "Protein kinase C
                        "Casein kinase II
                                            "Amidation
                                                             "Protein kinase C
                                                                               *Protein kinase C
                                                                                                 "N-myristoylation
                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                    "Protein kinase C phosphorylation
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The invention relates to polypeptide and polynucleotide of calpain-like CC protease, 18036. The polypeptide and polynucleotide of the invention are CC useful for treatment and diagnosis of calpain-like protease-mediated CC disorders. These disorders include disorders of spleen (e.g. disorders. These disorders include disorders of spleen (e.g. polynomegaly), lung (e.g. adult respiratory distress syndrome), colon CC (e.g. disopathic inflammatory bowel disease), liver (e.g. jaundice), CC brain (e.g. traumatic brain injury, cerebral oedema, cerebrovascular CC disease, acute meningitis, Alzheimer's disease), T-cells (e.g. transplant CC rejection, systemic lupus erythematosus), skin (e.g. sebornhoeic CC keratoses), haematopoietic stem cells (e.g. leukaemias), heart (e.g. cC myocardial infarction, atherosclerosis), kidney (e.g. acute proliferative CC glomerulonephritis, urolithiasis), thymus, breast, testis, uterus, cepididymis, endometrium; prostate, thyroid, skeletal muscle, pancreas, CC small intestine, disorders related to reduced platelet number, bone, CC ovary, pain and infectious disorders. The molecules of the invention are also useful for diagnosing and treating disorders associated with CC perturbed cellular growth and differentiation, exercise-induced injury CC demyelinating diseases including experimental allergic encephalomyelitis (EAE) and multiple sclerosis, Lomba neurodegenerative diseases, cancer and cell death associated with diverse toxicants. The present sequence consumed to between DSS140 and DSS2338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New calpain-like protease polypeptides and polynucleotides for diagnosing, treating seven-transmembrane protein/receptor-related disorders and to identify modulators of therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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467..469
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349..354
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Sequence
517 AA;
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D2S140

and D2S2338.

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Query Match
Best Local
                                                                                              Matches
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                                                      1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP
{\tt mragrgatparelfrdaafpaadsslfcdlstplaqfreditwrrpqeicatprlfpddp}
                                                                                             al Similarity
517; Conserve
                                                                                             Conservative
                                                                                                      74.5%;
                                                                                            0
                                                                                         Score 2719.5; DB 22;
Pred. No. 2.1e-238;
0; Mismatches 0; ]
                                                                                         Indels 155;
                                                                                                              Length
                                                                                        Gaps
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WO200023603-A2 Homo sapiens

15-AUG-2000

AAY79569;

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21-OCT-1999; 27-APR-2000

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readily detectable in many tissues, including skeletal muscle and islets. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A G-to-A polymorphism in intron 3 of the CAPNIO gene (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based on detection of a polymorphism in a 2 diabetes mellitus are based on detection of a polymorphism in a 2 calpain encoding nucleic caid, especially UCSNP-10 of the CAPNIO gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polynucleotides; regulating 2 diabetes by providing a calpain 10-encoding polynucleotides; regulating 2 diabetes by providing a calpain polypeptide such as calpain 10; polypeptides; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response
                                                                                                                                                                                             The present sequence is that of a novel human cysteine protease, designated calpain 10b. The protein is encoded by a transcript (see AAA2747) of the human calpain 10 gene, CARN10 (see AAA2747) which has been identified in the NIDDM1 region of chromosome 2. The CARN10 gene consists of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10h, respectively. Calpain 10b is
                                                                                                                                                                                                                                                                                                                            Claim 40; Page 220-222; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                   Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -
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13-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; calpain 10b; diapain-1; cysteine protease; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY79568 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bell GI;
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99US-0134175.
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Best Local Similarity
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                                FLLRVFSTGRVSLSAIRAVAK-----
                                                                            FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV
                                                                                                    REGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV
                                                                                                                                                                                                                                                                             {\tt mragrgatparelfrdaafpaadsslfcdlstplaqfreditwrrpqeicatprlfpddp}
fllrvfstgrvslralapaasaslcistagpvtpsstpsasi 522
                                                                                                                                                        IVSDLRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGE
                                                                                                                                                                                                                                             regqvkqgllgdcwflcacaalqksrhlldqvippgqpswadqeyrgsftcriwqfgrwv
                                                                    fpsnpkfwlrvsepsevyiavlqrsrlhaadwagraralvgdshtswspasipgkhyqav
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                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 9.6
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                  -NTTPGAAL 509
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RESULT
AAY79570
21-OCT-1998;
13-MAY-1999;
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                                        21-OCT-1999;
                                                                    27-APR-2000
                                                                                             W0200023603-A2
                                                                                                                       Homo sapiens
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980S-0105052
990S-0134175
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                                                                                                                                                                                                                                                                                       Protein;
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diagnosis;

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Method for screening for type 2 diabetes mellitus comprises detecting a polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -Threates out and the teacher of genes responsible for type of diabetes for use in diagnostication of genes responsible for type of diabetes for use in diagnostic and therapeutic applications. A construction of polymorphism in intron 3 of the CAPNIO gene (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed methods for creening for a propensity for type 2 diabetes mellitus are based of diabetes of a polymorphism in a calpain encoding nucleic acid, especially UCSNP-10 of the CAPNIO gene. Methods are also claimed for: producing calpain 10 polymorptides using calpain 10-encoding polymorlectides; regulating diabetes by providing a calpain oplymorptide such as calpain 10 polymorptides; identifying modulators of calpain activity using calpain 10 polymorptides; and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport. The present sequence is that of a novel human cysteine protease, designated calpain 10d. The protein is encoded by a transcript (see AAA27479) of the human calpain 10 gene, CAPN10 (see AA27475), which has been identified in the NIDDM1 region of chromosome 2. The CAPN10 gene consists of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 6517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10b, respectively. Calpain 10d is expressed only at 10v levels in the tissues examined. The Otan1 K; Zhou Y, Sreenan S, Claim 40; Page 225-227; 257pp; English. oda N, WPI; 2000-339702/29. N-PSDB; AAA27475, AAA27479. i, Horikawa Y, Bell GI: Polonsky Kš, Hanis CL, B 

513 AA; Sequence

ó REGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 120 EVITDDRIPCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLIGG 180 420 420 GLHLWKVEKRRVNLPRVLSMPPVAGTACHAYDREVHLRCELSPGYYLAVPSTFLKDAPGE 480 Gaps 1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP 361 FPSNPKFWLRVSEPSEVYIAVLQRSRLHAADWAGRARALVGDSHTSWSPASIPGKHYQAV ö Score 2699; DB 21; Length 513; Pred. No. 1.5e-236; 1; Mismatches 8; Indels 0; Indels 74.0%; ilarity 98.2%; Conservative Similarity Best Local Sim Matches 496; Query Match 61 121 301 301 361 421 셤 à g g a a ò ð à 8 ò ð ç 쉽 ò

treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport

Length 444;

Score 2336; DB 21; Pred. No. 1.2e-203;

64.0%; 99.8%;

Query Match Best Local Similarity

444 AA;

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The present sequence is that of a novel human cysteine protease, designated calpain 10e. The protein is encoded by a transcript (see AAA7480) of the human calpain 10 sene, CAPRIO (see AA27480) of the human calpain 10 sene, CAPRIO (see AA27475), which has been identified in the NIDDMI region of chromosome 2.

The CAPNIO gene consists of 15 exons spanning 32 kb. A complex pettern of alternative splicing generates proteins of 672, 544, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), designated calpain 10a to 10h, respectively. Calpain 10e is cypressed only at low levels in the tissues examined. The invention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A c-to-A-pulymorphism in intron 3 of the CAPRNO gene (UCSNP-43) shows evidence for linkage to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based of decrease in a calpain encoding nucleic acid, especially UCSNP-10 of the CAPRNO gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding polypeptide such as calpain 10e; identifying modulators of calpain coling calpain 10 polypeptides; and using these modulators contractory reserves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment -
                                                                                                                                                                                                                                                NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; calpain 10e; diapain-1; cystelne protease; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Otan1 K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sreenan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 40; Page 228-229; 257pp; English.
481 FLLRVFSTGRVSLSAIRAVAKNTTP 505
                   AAY79571 standard; Protein; 444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oda N,
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                                                                                                                                                                                 15-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horikawa Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polonsky KS, Hollinger, Gr. Bell GI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-339702/29
                                                                                                                                                                                                                  Human calpain 10e.
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                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                AAY79571;
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AAY 79571
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MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP Matches

425;

Conservative

1;

Mismatches

0;

Indels

0;

Gaps

0;

60 60

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RESULT 1
AAN25421
ID AAN2
XX AAN2
AC AAN2
XX Huma
XX Huma
XX Huma
XX Huma
KW Anti
KW Anti
KW Anti
KW Imwu
KW Anti
KW Geard
KW Geard
KW Huma
KW Imwu
KW Anti
KW Imwu
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                                                                                                                                                                                                                                                                                                                                                           W Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
W antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
W antibacterial; endocrine; cardiant; central nervous system; virucide;
W anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
W antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; ecrema;
W dermatological; antiallergic; antiasthmatic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
W genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaemia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW alzheimer's disease; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                         23-DEC-1999;
21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                     neurological
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                         990S-0471275.
2000US-0488725.
2000US-0552317.
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Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, Hry and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells they are expressed in, such as: antiinflammatory; antirheumaticantiarthritic; immunosuppressive; antibacterial; endocrine; cardiant central nervous system; virucide; anti-HTV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antilicer; osteopathic; dermatological; antialiergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 201; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer,
       172
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                                                                         121
                                                                                                            180
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                                                                                                                                                                                                          GLAERWNIKGVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARELGEFHA
                                    FIVSDLRELQGQAGQ
                                                                    glaerwnlkgvagsggggdrpgrwehrtcrqllhlkdqclisccvlsprag
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                                                                                                                                                                                                                                                                                                                                                                              245 AA;
eargqhgr 179
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                     26.4%;
89.7%;
                                      254
                                                                                                                                                                                                                                                                                  Score 964; DB 22;
Pred. No. 3.2e-79;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, useful for ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                     Length 245;
                                                                                                                                                                                                                                                                                    Indels
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RESULT 11
AAY79572
                  NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; calpain 10f; diapain-1; cysteine protease; diagno therapy.
                                                         Human calpain 10f
                                                                                15-AUG-2000
                                                                                                      AAY79572;
                                                                                                                        AAY79572 standard; Protein;
                                                                               (first entry)
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Homo sapiens

AAB62155 standard; Protein; 686 AA.

(first entry)

29-MAY-2001

AAB62155;

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The present sequence is that of a novel human cysteine protease, designated calpain 10f. The protein is encoded by a transcript (see AAZA7481) of the human calpain 10 gene, CARNIO (see AAZ7475), which has been identified in the NiDDMI region of chromosome 2.

"The CARNIO gene consists of 15 exons spanning 32 kb. A complex pattern of alternative splicing generates proteins of 672, 544, 517, 513, 444, 274, 139 and 138 amino acids (see AAY79567-74), expressed only at low levels in the tissues examined. The invention concerns the identification of genes responsible for type civention concerns the identification of genes responsible for type civention concerns the identification of genes responsible for type 2 diabetes for use in diagnostic and therapeutic applications. A general propensity for type 2 diabetes mellitus are based confection of a polymorphism in a calpain encoding nucleic acid, especially UCSNP-10 of the CARNIO gene. Methods for acid especially UCSNP-10 of the CARNIO gene. Methods are also claimed for: producing calpain 10 polypeptides using calpain 10-encoding colympatics such as calpain 10; identifying modulators of calpain activity using calpain 10 polypeptides; and using these modulators to respect transport.
                                                                                                                                                                                                                                                                                                                                detecting a
                                                                                                                                                                                                                Oda N, Sreenan S, Zhou Y, Otani K;
                                                                                                                                                                                                                                                                                                                              type 2 diabetes mellitus comprises concoding nucleic acid segment or a
                                                                                                                                                                                                                                                                                                                       for screening for type 2 diabetes mellitus
                                                                                                                                                                                                                                                                                                                                        Polymorphism in a calpain encoding nuclei
Protease-encoding nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                        Claim 40; Page 230-231; 257pp; English.
                                                                                        99WO-US24890.
                                                                                                                         98US-0105052.
                                                                                                                                                                                                                                                                                N-PSDB; AAA27475, AAA27481.
                                                                                                                                                                                                                S, Horikawa Y,
Bell GI;
                                                                                                                                                                           (ARCH-) ARCH DEV CORP.
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              WO200023603-A2
                                                                                      21-OCT-1999;
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Hanis CL,
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REGOVROGILGDCWFI.CACAALQKSRHILLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWV 120 EVITDDRLPCLAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGG 180 Gaps 1 MRAGRGATPARELFRDAAFPAADSSLFCDLSTPLAQFREDITWRRPQEICATPRLFPDDP 60 23; DB 21; Length 274; 13; Indels Score 858.5; DB 2. Pred. No. 1.5e-69; 1; Mismatches 13 181 · LAERWNLKGVAGSGGQQDRPGR 202 ----gcpggpdrrpgr 179 Query Match 23.5%; Best Local Similarity 81.7%; Matches 165; Conservative 19 121 168 g ð 셤 ö 合 ç 용 ò

RESULT 12 AAB62155

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The invention relates to novel human polynucleotides encoding protein

(NHP) that share sequence similarity with human calcium dependant

proteases. Nuclocided constructs encoding functional NHPs are used in

gene therapy for the modulation of NHP expression. NHP oligonucleotides

can be used as hybridization probes for screening libraries and assessing

the expression patterns. The sequences may also be used as part of

ribozyme and/or triple helix sequences that are useful for NHP gene

regulation. Labeled NHP nucleotide probes can be used to screen a human

genomic library. The NHP nucleotide sequences are also useful in drug

screening techniques. Nucleotide constructs encoding NHP products can be

used to genetically engineer host cells to express NHP products in vivo,

these genetically engineered cells function as bioreactors in the body,

delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion

protein to the body. The present sequence represents a NHP.
                                                                                                                                                                                                                                                                                                                                                                                                          Sands AT;
                                                                                                                                          Novel human protein; NHP; calcium; protease; gene therapy; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polynucleotides isolated from human testis cDNA library, encodes novel human proteins, useful as reagents in screening for compounds used for treating mental and biological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                      Zambrowicz B,
                                                                                                                                                                                                                                                                                                                                                                                                    Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 33-35; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Nehls M,
                                                                                                      Novel human protein (NHP) #4.
                                                                                                                                                                                                                                                                                                                                                               (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                      01-SEP-2000; 2000WO-US24062.
                                                                                                                                                                                                                                                                                                                           99US-0152057.
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N-PSDB; AAF57305.
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                                                                                                                                                                                                                 WO200116336-A1.
                                                                                                                                                                                 Homo sapiens.
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GDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPC 130 131 LAGRICFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGV 190 191 AGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARE-----LGEFHAFIVSD 244 265 245 LRELQCQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSOLQEGEFWVE 304 Gaps 12 ELFRDAAFPAADSSL-FCDLSTPLAQFREDITWRRPQEICATPRLFPDDPREGQVKQGLL 70 DB 22; Length 686; 17.7%; Score 644.5; DB 2 33.7%; Pred. No. 1.7e-49; tive 71; Mismatches 201 : | | | | | | | | | | | | Query Match
Best Local Similarity 33.77
Matches 168; Conservative 71

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RESULT 13
AAB40701
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                                                                               Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                N-PSDB; AAC74910.
                                                                                                                                                                                                                                                                     02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                     31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                         (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                             W0200058473-A2
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485 1pstfephrdadfllrvft 503
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                                                                                                                                                                2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     damage; cartilage damage; antiinflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEFLREFDELTVG--YPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG-F
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397. which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary.

Claim

11;

Page 929-931;

5507pp; English

XEXEXEX

06-NOV-2001 AAM79025;

(first

Human protein SEQ ID NO 1687

RESULT 14

AAM79025 standard;

Protein;

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Best Local Sin
Matches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX associated disorder. The
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osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
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                                      469 VPSTFLKDAPGEFLLRVFS 487
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                                                                      \tt qlqtigfvlyavpkefqniqdvhlkkefftkyqdhgfseiftnsrevssqlrlppgeyii
                                                                                                      HYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAY-----DREVHLRCELSPGYYLA 468
ipstfephrdadfllrvft 503
                                                                                                                                                                                        PSNPKFWLRVSE---PSEVYIAVLQRSRLHAADWAGR---ARALVGDSHTSWSPASIPGK
                                                                                                                                                                                                                           yqdflnnftlleicnltpdtlsgdyksyw-----httfyegswrrgssaggcrnhpgtf
                                                                                                                                                                                                                                                                                                                                                                                                                       AGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGARE-----LGEFHAFIVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAGRLCFSRCQREDVFWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gdcwllaaigslttcpkllyrvvprgqs--fkknyagifhfqiwqfgqwvnvvvddrlpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elfedplfpaepsslgfkdlg-pnsknvqniswqrpkdiinnplfimdgisptdicqgil
                                                                                                                                                                                                                                                                   EEEFLREFDELTVG--YPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%; Score 644.5; DB 21; 33.7%; Pred. No. 1.7e-49; tive 71; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -daegnvvvctclvalmgknwrharqqga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder. The
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or transmentance.
Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                        ı C,
Wang 7
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Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 4033-4034; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in diagnosis and gene therapy
                                                                                                                                                                                                                                             20000S-0620325.
20000S-0654936.
20000S-0663561.
20000S-0693325.
                                                                                                                                                                    05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                          HYSE-) HYSEQ INC.
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                                                                                                          WO200157190-A2.
                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                            30-NOV-2000;
                                                                                                                                                                                                                                                                             15-SEP-2000;
                                                                                                                                                                                                                    27-APR-2000;
20-JUN-2000;
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                                                                                                                                                                                                    03-FEB-2000;
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                                                                                                                                         09-AUG-2001
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Zhao QA,
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                                                                                                      GDCWFLCACAALQKSRHLLDQVIPPGQPSWADQEYRGSFTCRIWQFGRWVEVTTDDRLPC 130
                                                                                                                                                       131 LAGRICFSRCQREDVFWLPLLERVYAKVHGSYEHLWAGQVADALVDLFGGLAERWNLKGV 190
                                                                                                                                                                      191 AGSGGOODRPGRWEHRTCROLLHLKDOCLISCCVLSPRAGARE-----LGEFHAFIVSD 244
                                                                                                                     Gaps
                                                  12 ELFRDAAFPAADSSL-FCDLSTPLAGFREDITWRRPQEICATPRLFPDDPREGQVKQGLL 70
                                                                  DB 22; Length 702;
                               Indels
17.7%; Score 644.5; DB 22;
33.7%; Pred. No. 1.7e-49;
ative 71; Mismatches 201;
Query Match
Best Local Similarity 33.7
Matches 168; Conservative
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                                                 LRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFWVE 304
                                                                                                                                                                                                                                                                                            Novel human protein; NHP; calcium; protease; gene therapy; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polynucleotides isolated from human testis cDNA library, encodes novel human proteins, useful as reagents in screening for compounds used for treating mental and biological disorders -
         305 EEEFLREFDELIVG--YPVTEAGHLQSLYTERLLCHTRALPGAWVKGQSAGGCRNNSG-F
                                                                                                              416 HYQAVGLHLWKVEKRRVNLPRV-LSMPPVAGTACHAY-----DREVHLRCELSPGYYLA
                                                                         362 PSNPKFWLRVSE---PSEVYIAVLQRSRLHAADWAGR---ARALVGDSHTSWSPASIPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                Zambrowicz B,
                                                                                                                                                                                                                                                                                                                                                                                                                              Friedrich G,
                                                                                                                                                                                                                   AAB62154 standard; Protein; 702 AA.
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                                                                                                                                                                                                                                                                           Novel human protein (NHP) #3:
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485 ipstfephrdadfllrvft 503
                                                                                                                                                  469 VPSTFLKDAPGEFLLRVFS 487
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                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Donoho G, Turner CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235112/24.
N-PSDB; AAF57304.
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The invention relates to novel human polynucleotides encoding protein (NHP) that share sequence similarity with human calcium dependant proteases. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression. NHP oligonucleotides can be used as hybridization probes for screening libraries and assessing NHP gene expression patterns. The sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. Labeled NHP nucleotide sequences are also useful in drug genemic library. The NHP nucleotide sequences are also useful in drug screening techniques. Nucleotide constructs encoding NHP products can be used to genetically engineer host cells to express NHP products in vivo, these genetically engineer dells function as bioreactors in the body, delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. The present sequence represents a NHP Claim 6; Page 31-33; 39pp; English.

A)

702

Sequence

```
Query Match 17.7%; Score 644.5; DB 22; Length 702; Best Local Similarity 33.7%; Pred. No. 1.7e-49; Matches 168; Conservative 71; Mismatches 201; Indels 59;
425 qlqtlgfvlyavpkefqnlqdvhlkkefftkyqdhgfselftnsrevssqlrlppgeyii 484
                                                                                                 416 HYQAVGLHLMKVEKRRYNLPRV-LSMPPVAGTACHAY-----DREVHLRCELSPGYYLA 468
                                                                                                                                                    325 yqdflnnftlleicnltpdtlsgdyksyw-----httfyegswrrgssaggcrnhpgtf 378
                                                                                                                                                                    266 lqdvh-yrgkmetlirvrnpwgriewngawsdsareweevasdiqmqllhktedgefwms 324
                                                                                                                                                                                                                       245 LRELQGQAGQCILLLRIQNPWGRRCWQGLWREGGEGWSQVDAAVASELLSQLQEGEFWVE 304
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